PATENT APPLICATION

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Docket No: 28341/6227.1NCP

PATENT APPLICATION TRANSMITTAL UNDER 37 C.F.R. 1.53

Box Patent Application
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith for filing is the patent application of

Inventor(s):   David E. Lowery, Troy E. Fuller and Michael J. Kennedy

Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

1.   Type of Application

☒   This is a new application for a

    ☒   utility patent.

    ☐   design patent.

☐   This is a continuation-in-part application of prior application no.

2.   Application Papers Enclosed

    1   Title Page

    53   Pages of Specification (excluding Claims, Abstract, Drawings & Sequence Listing)

    8   Page(s) of Claims

    1   Page(s) of Abstract

    0   Sheet(s) of Drawings (Figs. ___ to ___)

        ☐   Formal

        ☐   Informal

    259   Page(s) of Sequence Listing

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Patent Application Transmittal and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on **April 6, 2000**, in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. EM362733684US.

Richard Zimmermann

3. Declaration or Oath

    ☐   Enclosed

        ☐   Executed by (check all applicable boxes)

            ☐   Inventor(s)

            ☐   Legal representative of inventor(s)
                    (37 CFR 1.42 or 1.43)

            ☐   Joint inventor or person showing a proprietary interest on
                    behalf of inventor who refused to sign or cannot be reached

                ☐   The petition required by 37 CFR 1.47 and the
                        statement required by 37 CFR 1.47 are enclosed. See
                        Item 5D below for fee.

    ☒   Not enclosed - the undersigned attorney or agent is authorized to file this
            application on behalf of the applicant(s). An executed declaration will follow.

4. Additional Papers Enclosed

    ☐   Preliminary Amendment

    ☐   Information Disclosure Statement

    ☐   Declaration of Biological Deposit

    ☒   Computer readable copy of sequence listing containing nucleotide and/or amino
            acid sequence ans statement under 37 C.F.R. §1.821

    ☐   Microfiche computer program

    ☐   Verified statement(s) claiming small entity status under 37 CFR 1.9 and 1.27

    ☐   Associate Power of Attorney

    ☐   Verified translation of a non-English patent application

    ☐   An assignment of the invention

    ☒   Return receipt postcard

    ☐   Other

5.   Priority Applications Under 35 USC 119

Certified copies of applications from which priority under 35 USC 119 is claimed are listed below

and

☐   are attached.

☐   will follow.

COUNTRY	APPLICATION NO.	FILED

6.   Filing Fee Calculation (37 CFR 1.16)

A.   ☒   **Utility Application**

CLAIMS AS FILED – INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		OTHER THAN A SMALL ENTITY	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				$345.00		$690.00
TOTAL	51 -20	= 31	X 9 =	$	X 18 =	$558.00
INDEP.	11 - 3	= 8	X 39 =	$	X 78 =	$624.00
☒ First Presentation of Multiple Dependent Claim			+ 130 =	$	+ 260 =	$260.00
			Filing Fee:	$	**OR**	$2,132.00

B.   ☐   **Design Application ($155.00/$310.00)**   Filing Fee: $ _____

C.   ☐   **Plant Application ($240.00/$480.00)**   Filing Fee: $ _____

D.   **Other Fees**

☐   Recording Assignment [Fee -- **$40.00** per assignment] $ _____

☐   Petition fee for filing by other than all the inventors
        or person on behalf of the inventor where inventor refused
        to sign or cannot be reached   [Fee -- **$130.00**] $ _____

☐   Other $ _____

Total Fees Enclosed $2,132.00

7.   Method of Payment of Fees

☒   Enclosed check in the amount of: $2,132.00

☐   Charge Deposit Account No. 13-2855 in the amount of: $_____
         A copy of this Transmittal is enclosed.

☐   Not enclosed

8.   Deposit Account and Refund Authorization

The Commissioner is hereby authorized to charge any deficiency in the amount enclosed or any additional fees which may be required during the pendency of this application under 37 CFR 1.16 or 37 CFR 1.17 or under other applicable rules (except payment of issue fees), to Deposit Account No. 13-2855. A copy of this Transmittal is enclosed.
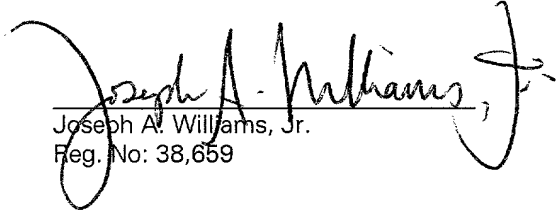
Please refund any overpayment to Marshall, O'Toole, Gerstein, Murray & Borun at the address below.

Please direct all future communications to Joseph A. Williams, Jr., at the address below.

Respectfully submitted,

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April 6, 2000

JOINT INVENTORS

APPLICATION FOR
UNITED STATES LETTERS PATENT

S P E C I F I C A T I O N

TO ALL WHOM IT MAY CONCERN:

Be it known that we, David E. Lowery a citizen of the United States of America, residing at 1207 Woodland Drive, Portage, 49024 in the County of Kalamazoo and State of Michigan and Troy E. Fuller a citizen of the United States of America, residing at 111 Dreamfield Drive, Battle Creek, 49014, in the County of Calhoun and State of Michigan and Michael J. Kennedy a citizen of the United States of America, residing at 2364 Quincy Avenue, Portage, 49024, in the County of Kalamazoo and State of Michigan have invented a new and useful ANTI-BACTERIAL VACCINE COMPOSITIONS, of which the following is a specification.

New Patent Application for: David E. Lowery, Troy E. Fuller, and Michael J. Kennedy

For: ANTI-BACTERIAL VACCINE COMPOSITIONS

Mailing Certification for: New Patent Application

Attorney Docket No: 28341/6227.1NCP

"EXPRESS MAIL" mailing label No. EM362733684US
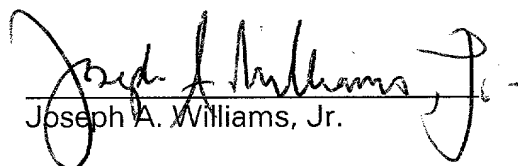
Date of Deposit: April 6, 2000

I hereby certify that this paper (or fee) is being deposited with the United States Postal Service "EXPRESS MAIL POST OFFICE TO ADDRESSEE" service under 37 CFR §1.10 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C., 20231.

Richard Zimmermann

Certificate of 37 C.F.R. §1.821 (f)

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R. §1.821(c) and (e), respectively, are the same.

Joseph A. Williams, Jr.

ANTI-BACTERIAL
VACCINE COMPOSITIONS

FIELD OF THE INVENTION

5   The present invention relates generally to the identification of genes responsible for virulence of *Pasteurella multocida* and *Actinobacillus pleuropneumoniae* bacteria, thereby allowing for production of novel attenuated mutant strains useful in vaccines and identification of new anti-bacterial agents that target the virulence genes and their products.

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BACKGROUND OF THE INVENTION

          The family *Pasteurellaceae* encompasses several significant pathogens that infect a wide variety of animals. In addition to *P. multocida*, prominent members of the family include *Pasteurella haemolytica, Actinobacillus pleuropneumoniae* and

15   *Haemophilus somnus*. *P. multocida* is a gram-negative, nonmotile coccobacillus which is found in the normal flora of many wild and domestic animals and is known to cause disease in numerous animal species worldwide [Biberstein, In M. Kilian, W. Frederickson, and E. L. Biberstein (ed.), *Haemophilus, Pasteurella, and Actinobacillus*. Academic Press, London, p. 61-73 (1981)]. The disease manifestations following

20   infection include septicemias, bronchopneumonias, rhinitis, and wound infections [Reviewed in Shewen, *et al., In* C. L. Gyles and C. O. Thoen (ed.), <u>Pathogenesis of Bacterial Infections in Animals</u>. Iowa State University Press, Ames, p. 216-225 (1993), incorporated herein by reference].

          Infection by *P. multocida* generally results from invasion during periods

25   of stress, but transmission may also occur by aerosol or contact exposure, or via flea and tick vectors. In fowl, *P. multocida* infection gives rise to acute to peracute septicemia, particularly prevalent in domestic turkeys and wild waterfowl under stress conditions associated with overcrowding, laying, molting, or severe climatic change. In cattle, a similar hemorrhagic septicemia follows infection and manifests conditions including high

30   fever and depression, generally followed by quick death. Transmission is most likely through aerosol contact, but infection can also arise during periods of significant climatic change. In rabbits, infection gives rise to recurring purulent rhinitis, generally followed by conjunctivitis, otitis media, sinusitis, subcutaneous abscesses, and chronic

bronchopneumonia. In severe infections, rabbit mortality arises from acute fibrinous bronchopneumonia, septicemia, or endotoxemia. Disease states normally arise during periods of stress. In pigs, common *P. multocida* disease states include atrophic rhinitis and bacterial pneumonia. Similar pneumonia conditions are also detected in dogs, cats, goats, and sheep. *P. multocida* is commonly detected in oral flora of many animals and is therefore a common contaminant in bite and scratch wounds.

P. multocida strains are normally designated by capsular serogroup and somatic serotype. Five capsular serogroups (A, B, D, E, and F) and 16 somatic serotypes are distinguished by expression of characteristic heat-stable antigens. Most strains are host specific and rarely infect more than one or two animals. The existence of different serotypes presents a problem for vaccination because traditional killed whole cell bacteria normally provide only serotype-specific protection. However, it has been demonstrated that natural infection with one serotype can lead to immunological protection against multiple serotypes [Shewen, *et al., In* C. L. Gyles and C. O. Thoen (Ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993)] and cross protection can also be stimulated by using inactivated bacteria grown *in vivo* [Rimler, *et al., Am J Vet Res. 42*:2117-2121 (1981)]. One live spontaneous mutant *P. multocida* strain has been utilized as a vaccine and has been shown to stimulate a strong immune response [Davis, *Poultry Digest. 20*:430-434 (1987), Schlink, *et al., Avian Dis. 31*(1):13-21 (1987)]. This attenuated strain, however, has been shown to revert to a virulent state or cause mortality if the vaccine recipient is stressed [Davis, *Poultry Digest. 20*:430-434 (1987), Schlink, *et al., Avian Dis. 31*(1):13-21 (1987)].

Another member of the *Pasteurella* family, *A. pleuropneumoniae* exhibits strict host specificity for swine and is the causative agent of highly contagious porcine pleuropneumonia. Infection normally arises in intensive breeding conditions, and is believed to occur by a direct mode of transmission. The disease is often fatal and, as a result, leads to severe economic loss in the swine producing industry. *A. pleuropneumoniae* infection may be chronic or acute, and infection is characterized by a hemorrhagic, necrotic bronchopneumonia with accompanying fibrinous pleuritis. To date, bacterial virulence has been attributed to structural proteins, including serotype-specific capsular polysaccharides, lipopolysaccharides, and surface proteins, as well as

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extracellular cytolytic toxins. Despite purification and, in some instances cloning, of these virulence factors, the exact role of these virulence factors in *A. pleuropneumoniae* infection is poorly understood.

Twelve serotypes of *A. pleuropneumoniae* have been identified based on antigenic differences in capsular polysaccharides and production of extracellular toxins. Serotypes 1, 5, and 7 are most relevant to *A. pleuropneumoniae* infection in the United States, while serotypes 1, 2, 5, 7, and 9 are predominant in Europe. There are at least three significant extracellular toxins of *A. pleuropneumoniae* that are members of the haemolysin family and are referred to as RTX toxins. RTX toxins are produced by many Gram negative bacteria, including *E. coli*, *Proteus vulgarisa*, and *Pasteurella haemolytica*, and the proteins generally share structural and functional characteristics. Toxins from the various serotypes differ, however, in host specificity, target cells, and biological activities.

The major *A. pleuropneumoniae* RTX toxins include ApxI, ApxII, and ApxIII. ApxI and ApxII have haemolytic activity, with ApxI being more potent. ApxIII shows no haemolytic activity, but is cytotoxic for alveolar macrophages and neutrophils. Most *A. pleuropneumoniae* serotypes produce two of these three toxins. For example, serotypes 1, 5, 9, and 11 express ApxI and ApxII, and serotypes 2, 3, 4, 6, and 8 express ApxII and ApxIII. Serotype 10, however, produces only ApxI, and serotypes 7 and 12 express only ApxII. Those *A. pleuropneumoniae* serotypes that produce both ApxI and ApxII are the most virulent strains of the bacteria.

The Apx toxins were demonstrated to be virulence factors in murine models and swine infection using randomly mutated wild type bacteria [Tascon, *et al.,* *Mol. Microbiol.* *14*:207-216 (1994)]. Other *A. pleuropneumoniae* mutants have also been generated with targeted mutagenesis to inactivate the gene encoding the AopA outer membrane virulence protein [Mulks and Buysee, *Gene* *165*:61-66 (1995)].

In attempts to produce vaccine compositions, traditional killed whole cell bacteria have provided only serotype-specific protection [MacInnes and Smart, *supra*], however, it has been demonstrated that natural infection with a highly virulent serotype can stimulate strong protective immunity against multiple serotypes [Nielsen, *Nord Vet Med.* *31*:407-13 (1979), Nielsen, *Nord Vet Med.* *36*:221-234 (1984), Nielsen, *Can J Vet*

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Res. 29:580-582 (1988), Nielsen, *ACTA Vet Scand. 15*:80-89 (1994)]. One defined live-attenuated vaccine strain producing an inactive form of the ApxII toxin has shown promise for cross protection in swine [Prideaux, *et al., Infection & Immunity 67*:1962-1966 (1999)], while other undefined live-attenuated mutants have also shown promise [Inzana, *et al., Infect Immun. 61*:1682-6, (1993), Paltineanu, et al., *In* International Pig Veterinary Society, 1992, p. 214, Utrera, *et al., In* International Pig Veterinary Society, 1992, p. 213].

Because of the problems associated with vaccine formulations comprising bacterial strains with undefined, spontaneous mutations, there exists a need in the art for rational construction of live attenuated bacterial strains for use in vaccines that will safely stimulate protective immunity against homologous and heterologous *P. multocida* and *A. pleuropneumoniae* serotypes. There further exists a need to identify attenuated bacterial strains and genes required for bacterial virulence, thereby facilitating development of methods to identify anti-bacterial agents.

SUMMARY OF THE INVENTION

In general, the present invention provides materials and methods for production and use of vaccine compositions comprising attenuated gram negative bacteria. In one aspect, vaccine compositions of the invention comprise attenuated species in the *Pasteurellaceae* family of bacteria, which is known in the art and described, in part, in Dewhirst, *et al., J. Bacteriol. 174*:2002-2013 (1992), incorporated herein by reference in its entirety. Species in the family include, but are not limited to, *A. actinomycetemcomitans, A. capsulatus, A. equuli, A. lignieresii, A. pleuropneumoniae (H. pleuropneumoniae), A. seminis, A. suis (H. suis), A. ureae (p. ureae), A. capsulatus,* Bisgaard taxon 11, *H. aegyptius, H. aphrophilus, H. aphrophilus (H. parainfluenzae), H. ducreyi, H.* haemoglobinophilus, *H. haemolyticus, H. influenzae, H. paracuniculus, H. paragallinarum, H. parahaemolyticus, H. parainfluenzae, (H. paraphrophilus), H. paraphrohaemolyticus, H. paraphrophilus, H. parasuis, H. parasuis* type 5, *H. segnis, H. somnus, Haemophilus* minor group, *Haemophilus* taxon C, *P. aerogenes, P. anatis, P. avium (H. avium), P. canis, P. dagmatis, P. gallinarum, P. haemolytica, P. trehalosi (P. haemolytica* biotype T), *P. langaa, P. multocida, P. pneumotropica, P. stomatis, P.*

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volantium (H. parainfluenzae), *P. volantium*, *Pasteurella* species A, *Pasteurella* species B, and *Haemophilus paraphrohaemolyticus*. Preferably, vaccine compositions comprise attenuated *Pasteurella haemolytica*, *Actinobacillus pleuropneumoniae*, *Haemophilus somnus*, or *Pasteurella multocida* bacteria. In a most preferred embodiment, vaccine compositions of the invention comprise attenuated *Pasteurella multocida* and *A. plueropneumoniae* bacterial strains.

One aspect of the invention provides gram negative bacterial organisms containing a functional mutation in a gene sequence represented by any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or species homologs thereof, wherein the mutation inhibits or abolishes expression and/or biological activity of an encoded gene product (*i.e.*, the polypeptide encoded by a gene); said functional mutation resulting in attenuated virulence of the bacterial strain. As understood in the art, species homologs include genes found in two or more different species which possess substantial polynucleotide sequence homology and possess the same, or similar, biological functions and/or properties. Preferably polynucleotide sequences which represent species homologs will hybridize under moderately stringent conditions, as described herein by example, and possess the same or similar biological activities and or properties. In another aspect, polynucleotides representing species homologs will share greater than about 60% sequence homology, greater than about 70% sequence homology, greater than about 80% sequence homology, greater than about 90% sequence homology or greater than about 95% sequence homology. Functional mutations that modulate (*i.e.,* increase or decrease) expression and/or biological activity of a gene product include insertions or deletions in the protein coding region of the gene itself or in sequences responsible for, or involved in, control of gene expression. Deletion mutants include those wherein all or part of a specific gene sequence is deleted. In one aspect, the mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene. In another

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aspect, the mutation results in an insertion in the gene, wherein the insertion causes decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene. Also contemplated are compositions, and preferably vaccine compositions, comprising mutated and attenuated gram negative bacterial organisms, optionally comprising a suitable adjuvant and/or a pharmaceutically acceptable diluent or carrier. In order for a modified strain to be effective in a vaccine formulation, the attenuation must be significant enough to prevent the pathogen from evoking severe clinical symptoms, but also insignificant enough to allow limited replication and growth of the bacteria in the host.

The invention also provides polynucleotides encoding gene products that are required for virulence in gram negative bacteria. Polynucleotides of the invention include DNA, such as complementary DNA, genomic DNA including complementary or anti-sense DNA, and wholly or partially synthesized DNA; RNA, including sense and antisense strands; and peptide nucleic acids as described, for example in Corey, *TIBTECH 15*:224-229 (1997). Virulence gene polynucleotides of the invention include those set forth in SEQ ID NOs:1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or species homologs thereof, polynucleotides encoding a virulence gene product encoded by a polynucleotide of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or a species homolog thereof, and polynucleotide that hybridize, under moderately to highly stringent conditions, to the noncoding strand (or complement) of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, species homologs thereof. The invention therefore comprehends gene sequences from *Pasteurellaceae* set out in SEQ ID NOs: 1,

3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, as well as related gene sequences from other gram negative

5 bacterial organisms, including naturally occurring (*i.e.*, species homologs) and artificially induced variants thereof. The invention also comprehends polynucleotides which encode polypeptides deduced from any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122,

10 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, and species homologs thereof. Knowledge of the sequence of a polynucleotide of the invention makes readily available every possible fragment of that polynucleotide. The invention therefore provides fragments of a polynucleotide of the invention.

15 The invention further embraces expression constructs comprising polynucleotides of the invention. Host cells transformed, transfected or electroporated with a polynucleotide of the invention are also contemplated. The invention provides methods to produce a polypeptide encoded by a polynucleotide of the invention comprising the steps of growing a host cell of the invention under conditions that permit,

20 and preferably promote, expression of a gene product encoded by the polynucleotide, and isolating the gene product from the host cell or the medium of its growth.

Identification of polynucleotides of the invention makes available the encoded polypeptides. Polypeptides of the invention include full length and fragment, or truncated, proteins; variants thereof; fusion, or chimeric proteins; and analogs,

25 including those wherein conservative amino acid substitutions have been introduced into wild-type polypeptides. Antibodies that specifically recognize polypeptides of the invention are also provided, and include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, as well as compounds that

30 include CDR sequences which specifically recognize a polypeptide of the invention. The

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invention also provides anti-idiotype antibodies immunospecific for antibodies of the invention.

According to another aspect of the invention, methods are provided for identifying novel anti-bacterial agents that modulate the function of gram negative bacteria virulence genes or gene products. Methods of the invention include screening potential agents for the ability to interfere with expression of virulence gene products encoded by the DNA sequences set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or species homologs thereof, or screening potential agents for the ability to interfere with biological function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, species homologs thereof, or the complementary strand thereof, followed by identifying agents that provide positive results in such screening assays. In particular, agents that interfere with the expression of virulence gene products include anti-sense polynucleotides and ribozymes that are complementary to the virulence gene sequences. The invention further embraces methods to modulate transcription of gene products of the invention through use of oligonucleotide-directed triplet helix formation.

Agents that interfere with the function of virulence gene products include variants of virulence gene products, binding partners of the virulence gene products and variants of such binding partners, and enzyme inhibitors (where the product is an enzyme).

Novel anti-bacterial agents identified by the methods described herein are provided, as well as methods for treating a subject suffering from infection with gram negative bacteria involving administration of such novel anti-bacterial agents in an amount effective to reduce bacterial presence.

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Numerous additional aspects and advantages of the invention will become apparent to those skilled in the art upon consideration of the following detailed description of the invention which describes presently prepared embodiments thereof.

DETAILED DESCRIPTION OF THE INVENTION

"Virulence genes," as used herein, are genes whose function or products are required for successful establishment and/or maintenance of bacterial infection in a host animal. Thus, virulence genes and/or the proteins encoded thereby are involved in pathogenesis in the host organism, but may not be necessary for growth.

"Signature-tagged mutagenesis (STM)," as used herein, is a method generally described in International Patent Publication No. WO 96/17951, incorporated herein by reference, and includes, for example, a method for identifying bacterial genes required for virulence in a murine model of bacteremia. In this method, bacterial strains that each have a random mutation in the genome are produced using transposon integration; each insertional mutation carries a different DNA signature tag which allows mutants to be differentiated from each other. The tags comprise 40 bp variable central regions flanked by invariant "arms" of 20 bp which allow the central portions to be co-amplified by polymerase chain reaction (PCR). Tagged mutant strains are assembled in microtiter dishes, then combined to form the "inoculum pool" for infection studies. At an appropriate time after inoculation, bacteria are isolated from the animal and pooled to form the "recovered pool." The tags in the recovered pool and the tags in the inoculum pool are separately amplified, labeled, and then used to probe filters arrayed with all of the different tags representing the mutants in the inoculum. Mutant strains with attenuated virulence are those which cannot be recovered from the infected animal, *i.e.,* strains with tags that give hybridization signals when probed with tags from the inoculum pool but not when probed with tags from the recovered pool. In a variation of this method, non-radioactive detection methods such as chemiluminescence can be used

Signature-tagged mutagenesis allows a large number of insertional mutant strains to be screened simultaneously in a single animal for loss of virulence. Screening nineteen pools of mutant *P. multocida* strains resulted in the identification of more than 60 strains with reduced virulence, many of which were confirmed to be attenuated in

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virulence by subsequent determination of an approximate LD_{50} for the individual mutants. Screening of *A. pleuropneumoniae* mutants resulted in identification of more than 100 strains having mutations in 35 different genes. Of these, mutations in 22 genes results in significantly attenuated *A. pleuropneumoniae* strains. The nucleotide sequence of the open reading frame disrupted by the transposon insertion was determined by sequencing both strands and an encoded amino acid sequence was deduced. Novelty of both the polynucleotide and amino acid sequences was determined by comparison of the sequences with DNA and protein database sequences.

The identification of bacterial, and more particularly *P. multocida* and *A. pleuropneumoniae* virulence genes provides for microorganisms exhibiting reduced virulence (*i.e.*, attenuated strains), which are useful in vaccines. Such microorganisms include *Pasteurellaceae* mutants containing at least one functional mutation inactivating a gene represented by any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164. The worker of ordinary skill in the art will realize that a "functional mutation" may occur in protein coding regions of a gene of the invention, as well as in regulatory regions that modulate transcription of the virulence gene RNA.

The worker of ordinary skill will also appreciate that attenuated *P. multocida* and *A. pleuropneumoniae* strains of the invention include those bearing more than one functional mutation. More than one mutation may result in additive or synergistic degrees of attenuation. Multiple mutations can be prepared by design or may fortuitously arise from a deletion event originally intended to introduce a single mutation. An example of an attenuated strain with multiple deletions is a *Salmonella typhimurium* strain wherein the *cya* and *crp* genes are functionally deleted. This mutant *S. typhimurium* strain has shown promise as a live vaccine.

Identification of virulence genes in *P. multocida* and *A. pleuropneumoniae* can provide information regarding similar genes, *i.e.*, species homologs, in other pathogenic species. As an example, identification of the *aroA* gene led to identification of conserved genes in a diverse number of pathogens, including *P. haemolytica*,

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Aeromonas hydrophila, Aeromonas salmonicida, Salmonella typhimurium, Salmonella enteritidis, Salmonella dublin, Salmonella gallanerum, Bordella pertussis, Yersinia entericolitica, Neisseria gonorrhoeae, and Bacillus anthracis. In many of these species, attenuated bacterial strains bearing mutations in the *aroA* gene have proven to be effective in vaccine formulations. Using the virulence genes sequences identified in *P. multocida,* similar or homologous genes can be identified in other organisms, particularly within the *Pasteurella* family, as well as *A. pleuropneumoniae* and *Haemophilus somnus.* Likewise, identification of *A. pleuropneumoniae* virulence genes can permit identification of related genes in other organisms. Southern hybridization using the *P. multocida* and *A. pleuropneumoniae* genes as probes can identify these related genes in chromosomal libraries derived from other organisms. Alternatively, PCR can be equally effective in gene identification across species boundaries. As still another alternative, complementation of, for example, a *P. multocida* mutant with a chromosomal library from other species can also be used to identify genes having the same or related virulence activity. Identification of related virulence genes can therefore lead to production of an attenuated strain of the other organism which can be useful as still another vaccine formulation. Examples of *P. multocida* genes that have been demonstrated to exist in other species (*e.g. P. haemolytica, A. pleuropneumoniae* and *H. somnus*) include genes *exbB, atpG, and pnp*

Attenuated *P. multocida* strains identified using STM are insertional mutants wherein a virulence gene has been rendered non-functional through insertion of transposon sequences in either the open reading frame or regulatory DNA sequences. In one aspect, therefore, the attenuated *P. multocida* strains, as well as other gram-negative mutant bacterial strains of the invention can bear one or more mutations which result in an insertion in the gene, with the insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene. These insertional mutants still contain all of the genetic information required for bacterial virulence and can possibly revert to a pathogenic state by deletion of the inserted transposon. Therefore, in preparing a vaccine formulation, it is desirable to take the information gleaned from the attenuated strain and create a deletion mutant strain wherein some, most, or all of the virulence gene sequence is

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removed, thereby precluding the possibility that the bacteria will revert to a virulent state. The attenuated *P. multocida* strains, as well as other gram-negative mutant bacterial strains of the invention therefore include those bearing one or more mutation which results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of the virulence gene.

The vaccine properties of an attenuated insertional mutant identified using STM are expected to be the same or similar to those of a bacteria bearing a deletion in the same gene. However, it is possible that an insertion mutation may exert "polar" effects on adjoining gene sequences, and as a result, the insertion mutant may possess characteristic distinct from a mutant strain with a deletion in the same gene sequence. Deletion mutants can be constructed using any of a number of techniques well known and routinely practiced in the art.

In one example, a strategy using counterselectable markers can be employed which has commonly been utilized to delete genes in many bacteria. For a review, see, for example, Reyrat, *et al., Infection and Immunity* 66:4011-4017 (1998), incorporated herein by reference. In this technique, a double selection strategy is often employed wherein a plasmid is constructed encoding both a selectable and counterselectable marker, with flanking DNA sequences derived from both sides of the desired deletion. The selectable marker is used to select for bacteria in which the plasmid has integrated into the genome in the appropriate location and manner. The counterselecteable marker is used to select for the very small percentage of bacteria that have spontaneously eliminated the integrated plasmid. A fraction of these bacteria will then contain only the desired deletion with no other foreign DNA present. The key to the use of this technique is the availability of a suitable counterselectable marker.

In another technique, the *cre-lox* system is used for site specific recombination of DNA. The system consists of 34 base pair *lox* sequences that are recognized by the bacterial *cre* recombinase gene. If the *lox* sites are present in the DNA in an appropriate orientation, DNA flanked by the *lox* sites will be excised by the *cre* recombinase, resulting in the deletion of all sequences except for one remaining copy of

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the *lox* sequence. Using standard recombination techniques, it is possible to delete the targeted gene of interest in the *P. multocida* or *A. pleuropneumoniae* genome and to replace it with a selectable marker (*e.g.*, a gene coding for kanamycin resistance) that is flanked by the *lox* sites. Transient expression (by electroporation of a suicide plasmid containing the *cre* gene under control of a promoter that functions in *P. multocida* or *A. pleuropneumoniae*) of the *cre* recombinase should result in efficient elimination of the *lox* flanked marker. This process would result in a mutant containing the desired deletion mutation and one copy of the *lox* sequences.

In another approach, it is possible to directly replace a desired deleted sequence in the *P. multocida* or *A. pleuropneumoniae* genome with a marker gene, such as green fluorescent protein (GFP), β-galactosidase, or luciferase. In this technique, DNA segments flanking a desired deletion are prepared by PCR and cloned into a suicide (non-replicating) vector for *P. multocida* or *A. pleuropneumoniae*. An expression cassette, containing a promoter active in *P. multocida* or *A. pleuropneumoniae* and the appropriate marker gene, is cloned between the flanking sequences. The plasmid is introduced into wild-type *P. multocida* or *A. pleuropneumoniae*. Bacteria that incorporate and express the marker gene (probably at a very low frequency) are isolated and examined for the appropriate recombination event (*i.e.*, replacement of the wild type gene with the marker gene).

The reduced virulence of these organisms and their immunogenicity may be confirmed by administration to a subject animal. While it is possible for an avirulent microorganism of the invention to be administered alone, one or more of such mutant microorganisms are preferably administered in a vaccine composition containing suitable adjuvant(s) and pharmaceutically acceptable diluent(s) or carrier(s). The carrier(s) must be "acceptable" in the sense of being compatible with the avirulent microorganism of the invention and not deleterious to the subject to be immunized. Typically, the carriers will be water or saline which will be sterile and pyrogen free. The subject to be immunized is a subject needing protection from a disease caused by a virulent form of *P. multocida*, *A. pleuropneumoniae*, or other pathogenic microorganisms.

It will be appreciated that the vaccine of the invention may be useful in the fields of human medicine and veterinary medicine. Thus, the subject to be

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immunized may be a human or other animal, for example, farm animals including cows, sheep, pigs, horses, goats and poultry (*e.g.*, chickens, turkeys, ducks and geese) companion animals such as dogs and cats; exotic and/or zoo animals; and laboratory animals including mice, rats, rabbits, guinea pigs, and hamsters.

5   The invention also provides polypeptides and corresponding polynucleotides required for *P. multocida* or *A. pleuropneumoniae* virulence. The invention includes both naturally occurring and non-naturally occurring polynucleotides and polypeptide products thereof. Naturally occurring virulence products include distinct gene and polypeptide species as well as corresponding species homologs

10   expressed in organisms other than *P. multocida* or *A. pleuropneumoniae* strains. Non-naturally occurring virulence products include variants of the naturally occurring products such as analogs and virulence products which include covalent modifications. In a preferred embodiment, the invention provides virulence polynucleotides comprising the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31,

15   33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof, and polypeptides having amino acids sequences encoded by the polynucleotides.

20   The present invention provides novel purified and isolated *P. multocida* and *A. pleuropneumoniae* polynucleotides (e.g., DNA sequences and RNA transcripts, both sense and complementary antisense strands) encoding the bacterial virulence gene products. DNA sequences of the invention include genomic and cDNA sequences as well as wholly or partially chemically synthesized DNA sequences. Genomic DNA of

25   the invention comprises the protein coding region for a polypeptide of the invention and includes variants that may be found in other bacterial strains of the same species. "Synthesized," as used herein and is understood in the art, refers to purely chemical, as opposed to enzymatic, methods for producing polynucleotides. "Wholly" synthesized DNA sequences are therefore produced entirely by chemical means, and "partially"

30   synthesized DNAs embrace those wherein only portions of the resulting DNA were produced by chemical means. Preferred DNA sequences encoding *P. multocida*

virulence gene products are set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. Preferred *A. pleuropneumoniae* DNA sequences encoding virulence gene products are set out in SEQ ID NOs: 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. The worker of skill in the art will readily appreciate that the preferred DNA of the invention comprises a double stranded molecule, for example, molecules having the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof, along with the complementary molecule (the "non-coding strand" or "complement") having a sequence deducible from the sequence of SEQ ID NO: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, according to Watson-Crick base pairing rules for DNA. Also preferred are polynucleotides encoding the gene products encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. The invention further embraces species, preferably bacterial, homologs of the *P. multocida* and *A. pleuropneumoniae* DNA.

The polynucleotide sequence information provided by the invention makes possible the identification and isolation of polynucleotides encoding related bacterial virulence molecules by well known techniques including Southern and/or Northern hybridization, and polymerase chain reaction (PCR). Examples of related polynucleotides include polynucleotides encoding polypeptides homologous to a

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virulence gene product encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof, and structurally related polypeptides sharing one or more biological and/or physical properties of a virulence gene product of the invention.

The invention also embraces DNA sequences encoding bacterial gene products which hybridize under moderately to highly stringent conditions to the non-coding strand, or complement, of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. DNA sequences encoding virulence polypeptides which would hybridize thereto but for the degeneracy of the genetic code are contemplated by the invention. Exemplary high stringency conditions include a final wash in buffer comprising 0.2X SSC/0.1% SDS, at 65°C to 75°C, while exemplary moderate stringency conditions include a final wash in buffer comprising 2X SSC/0.1% SDS, at 35°C to 45°C. It is understood in the art that conditions of equivalent stringency can be achieved through variation of temperature and buffer, or salt concentration as described in Ausubel, *et al.* (Eds.), Protocols in Molecular Biology, John Wiley & Sons (1994), pp. 6.0.3 to 6.4.10. Modifications in hybridization conditions can be empirically determined or precisely calculated based on the length and the percentage of guanosine/cytosine (GC) base pairing of the probe. The hybridization conditions can be calculated as described in Sambrook, *et al.*, (Eds.), Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York (1989), pp. 9.47 to 9.51.

Autonomously replicating recombinant expression constructions such as plasmid and viral DNA vectors incorporating virulence gene sequences are also provided. Expression constructs wherein virulence polypeptide-encoding polynucleotides are operatively linked to an endogenous or exogenous expression control DNA sequence and

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a transcription terminator are also provided. The virulence genes may be cloned by PCR, using *P. multocida* genomic DNA as the template. For ease of inserting the gene into expression vectors, PCR primers are chosen so that the PCR-amplified gene has a restriction enzyme site at the 5′ end preceding the initiation codon ATG, and a restriction

5   enzyme site at the 3′ end after the termination codon TAG, TGA or TAA. If desirable, the codons in the gene are changed, without changing the amino acids, according to *E. coli* codon preference described by Grosjean and Fiers, *Gene, 18*:199-209 (1982), and Konigsberg and Godson, *Proc. Natl. Acad. Sci. (USA), 80*:687-691 (1983). Optimization of codon usage may lead to an increase in the expression of the gene product when

10   produced in *E. coli*. If the gene product is to be produced extracellularly, either in the periplasm of *E. coli* or other bacteria, or into the cell culture medium, the gene is cloned without its initiation codon and placed into an expression vector behind a signal sequence.

         According to another aspect of the invention, host cells are provided,

15   including procaryotic and eukaryotic cells, either stably or transiently transformed, transfected, or electroporated with polynucleotide sequences of the invention in a manner which permits expression of virulence polypeptides of the invention. Expression systems of the invention include bacterial, yeast, fungal, viral, invertebrate, and mammalian cells systems. Host cells of the invention are a valuable source of immunogen for

20   development of antibodies specifically immunoreactive with the virulence gene product. Host cells of the invention are conspicuously useful in methods for large scale production of virulence polypeptides wherein the cells are grown in a suitable culture medium and the desired polypeptide products are isolated from the cells or from the medium in which the cells are grown by, for example, immunoaffinity purification or any of the multitude

25   of purification techniques well known and routinely practiced in the art. Any suitable host cell may be used for expression of the gene product, such as *E. coli*, other bacteria, including *P. multocida, Bacillus* and *S. aureus*, yeast, including *Pichia pastoris* and *Saccharomyces cerevisiae*, insect cells, or mammalian cells, including CHO cells, utilizing suitable vectors known in the art. Proteins may be produced directly or fused

30   to a peptide or polypeptide, and either intracellularly or extracellularly by secretion into the periplasmic space of a bacterial cell or into the cell culture medium. Secretion of a

protein requires a signal peptide (also known as pre-sequence); a number of signal sequences from prokaryotes and eukaryotes are known to function for the secretion of recombinant proteins. During the protein secretion process, the signal peptide is removed by signal peptidase to yield the mature protein.

5   To simplify the protein purification process, a purification tag may be added either at the 5′ or 3′ end of the gene coding sequence. Commonly used purification tags include a stretch of six histidine residues (U.S. Patent Nos. 5,284,933 and 5,310,663), a streptavidin-affinity tag described by Schmidt and Skerra, *Protein Engineering*, 6:109-122 (1993), a FLAG peptide [Hopp *et al.*, *Biotechnology*, 6:1205-
10   1210 (1988)], glutathione S-transferase [Smith and Johnson, *Gene*, 67:31-40 (1988)], and thioredoxin [LaVallie *et al.*, *Bio/Technology*, 11:187-193 (1993)]. To remove these peptide or polypeptides, a proteolytic cleavage recognition site may be inserted at the fusion junction. Commonly used proteases are factor Xa, thrombin, and enterokinase.

The invention also provides purified and isolated *P. multocida* and *A.*
15   *pleuropneumoniae* virulence polypeptides encoded by a polynucleotide of the invention. Presently preferred are polypeptides comprising the amino acid sequences encoded by any one of the polynucleotides set out in SEQ ID NOs : 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132,
20   134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, and species homologs thereof. The invention embraces virulence polypeptides encoded by a DNA selected from the group consisting of : a) the DNA sequence set out in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114,
25   116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, and species homologs thereof; b) DNA molecules encoding *P. multocida* or *A. pleuropneumoniae* polypeptides encoded by any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110,
30   112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, and species homologs thereof; and

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c) a DNA molecule, encoding a virulence gene product, that hybridizes under moderately stringent conditions to the DNA of (a) or (b).

The invention also embraces polypeptides, *i.e.,* species homologs and orthologs, that have at least about 99%, at least about 95%, at least about 90%, at least about 85%, at least about 80%, at least about 75%, at least about 70%, at least about 65%, at least about 60%, at least about 55%, and at least about 50% identity and/or homology to the preferred polypeptides of the invention. Percent amino acid sequence "identity" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in the virulence gene product sequence after aligning both sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Percent sequence "homology" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in one of the virulence polypeptide sequences after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and also considering any conservative substitutions as part of the sequence identity. Conservative substitutions can be defined as set out in Tables A and B.

Table A
Conservative Substitutions I

SIDE CHAIN CHARACTERISTIC		AMINO ACID
Aliphatic	Non-polar	G A P
		I L V
	Polar - uncharged	C S T M
		N Q
	Polar - charged	D E
		K R
Aromatic		H F W Y
Other		N Q D E

Polypeptides of the invention may be isolated from natural bacterial cell sources or may be chemically synthesized, but are preferably produced by recombinant

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procedures involving host cells of the invention. Virulence gene products of the invention may be full length polypeptides, biologically active fragments, or variants thereof which retain specific biological or immunological activity. Variants may comprise virulence polypeptide analogs wherein one or more of the specified (*i.e.*, naturally encoded) amino acids is deleted or replaced or wherein one or more non-specified amino acids are added: (1) without loss of one or more of the biological activities or immunological characteristics specific for the virulence gene product; or (2) with specific disablement of a particular biological activity of the virulence gene product. Deletion variants contemplated also include fragments lacking portions of the polypeptide not essential for biological activity, and insertion variants include fusion polypeptides in which the wild-type polypeptide or fragment thereof have been fused to another polypeptide.

Variant virulence polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Conservative substitutions are recognized in the art to classify amino acids according to their related physical properties and can be defined as set out in Table A (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96). Alternatively, conservative amino acids can be grouped as defined in Lehninger, [Biochemistry, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77] as set out in Table B.

Table B
Conservative Substitutions II

SIDE CHAIN CHARACTERISTIC	AMINO ACID
Non-polar (hydrophobic)	
A. Aliphatic:	A L I V P
B. Aromatic:	F W
C. Sulfur-containing:	M
D. Borderline:	G
Uncharged-polar	
A. Hydroxyl:	S T Y
B. Amides:	N Q
C. Sulfhydryl:	C
D. Borderline:	G
Positively Charged (Basic):	K R H
Negatively Charged (Acidic):	
DE	

Variant virulence products of the invention include mature virulence gene products, *i.e.*, wherein leader or signal sequences are removed, having additional amino terminal residues. Virulence gene products having an additional methionine residue at position -1 are contemplated, as are virulence products having additional methionine and lysine residues at positions -2 and -1. Variants of these types are particularly useful for recombinant protein production in bacterial cell types. Variants of the invention also nclude gene products wherein amino terminal sequences derived from other proteins have been introduced, as well as variants comprising amino terminal sequences that are not found in naturally occurring proteins.

The invention also embraces variant polypeptides having additional amino acid residues which result from use of specific expression systems. For example, use of commercially available vectors that express a desired polypeptide as a fusion protein with glutathione-S-transferase (GST) provide the desired polypeptide having an additional glycine residue at position -1 following cleavage of the GST component from the desired polypeptide. Variants which result from expression using other vector systems are also contemplated.

Also comprehended by the present invention are antibodies (*e.g.*, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies,

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humanized, human, and CDR-grafted antibodies, including compounds which include CDR sequences which specifically recognize a polypeptide of the invention) and other binding proteins specific for virulence gene products or fragments thereof. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind a virulence polypeptide exclusively (*i.e.*, are able to distinguish a single virulence polypeptides from related virulence polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Harlow *et al.* (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor , NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the virulence polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, a virulence polypeptide of the invention from which the fragment was derived.

The DNA and amino acid sequence information provided by the present invention also makes possible the systematic analysis of the structure and function of the virulence genes and their encoded gene products. Knowledge of a polynucleotide encoding a virulence gene product of the invention also makes available anti-sense polynucleotides which recognize and hybridize to polynucleotides encoding a virulence polypeptide of the invention. Full length and fragment anti-sense polynucleotides are provided. The worker of ordinary skill will appreciate that fragment anti-sense molecules of the invention include (i) those which specifically recognize and hybridize to a specific RNA (as determined by sequence comparison of DNA encoding a virulence polypeptide of the invention to DNA encoding other known molecules) as well as (ii) those which recognize and hybridize to RNA encoding variants of the family of virulence proteins. Antisense polynucleotides that hybridize to RNA encoding other members of the virulence family of proteins are also identifiable through sequence comparison to identify characteristic, or signature, sequences for the family of molecules.

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The invention further contemplates methods to modulate gene expression through use of ribozymes. For a review, see Gibson and Shillitoe, *Mol. Biotech. 7*:125-137 (1997). Ribozyme technology can be utilized to inhibit translation of mRNA in a sequence specific manner through (i) the hybridization of a complementary RNA to a target mRNA and (ii) cleavage of the hybridized mRNA through nuclease activity inherent to the complementary strand. Ribozymes can be identified by empirical methods but more preferably are specifically designed based on accessible sites on the target mRNA [Bramlage, *et al., Trends in Biotech 16*:434-438 (1998)]. Delivery of ribozymes to target cells can be accomplished using either exogenous or endogenous delivery techniques well known and routinely practiced in the art. Exogenous delivery methods can include use of targeting liposomes or direct local injection. Endogenous methods include use of viral vectors and non-viral plasmids.

Ribozymes can specifically modulate expression of virulence genes when designed to be complementary to regions unique to a polynucleotide encoding a virulence gene product. "Specifically modulate" therefore is intended to mean that ribozymes of the invention recognizes only a single polynucleotide. Similarly, ribozymes can be designed to modulate expression of all or some of a family of proteins. Ribozymes of this type are designed to recognize polynucleotide sequences conserved in all or some of the polynucleotides which encode the family of proteins.

The invention further embraces methods to modulate transcription of a virulence gene of the invention through use of oligonucleotide-directed triplet helix formation. For a review, see Lavrovsky, *et al., Biochem. Mol. Med. 62*:11-22 (1997). Triplet helix formation is accomplished using sequence specific oligonucleotides which hybridize to double stranded DNA in the major groove as defined in the Watson-Crick model. Hybridization of a sequence specific oligonucleotide can thereafter modulate activity of DNA-binding proteins, including, for example, transcription factors and polymerases. Preferred target sequences for hybridization include transcriptional regulatory regions that modulate virulence gene product expression. Oligonucleotides which are capable of triplet helix formation are also useful for site-specific covalent modification of target DNA sequences. Oligonucleotides useful for covalent

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modification are coupled to various DNA damaging agents as described in Lavrovsky, *et al.* [*supra*].

The identification of *P. multocida* and *A. pleuropneumoniae* virulence genes renders the genes and gene products useful in methods for identifying anti-bacterial agents. Such methods include assaying potential agents for the ability to interfere with expression of virulence gene products represented by the DNA sequences set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof (*i.e.*, the genes represented by DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, encode the virulence gene product, or the DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, are adjacent the gene encoding the virulence gene product, or are involved in regulation of expression of the virulence gene product), or assaying potential agents for the ability to interfere with the function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, species homologs thereof, or the complementary strand thereof, followed by identifying agents that are positive in such assays. Polynucleotides and polypeptides useful in these assays include not only the genes and encoded polypeptides as disclosed herein, but also variants thereof that have substantially the same activity as the wild-type genes and polypeptides.

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The virulence gene products produced by the methods described above are used in high throughput assays to screen for inhibitory agents. The sources for potential agents to be screened are chemical compound libraries, fermentation media of *Streptomycetes*, other bacteria and fungi, and cell extracts of plants and other vegetations. For proteins with known enzymatic activity, assays are established based on the activity, and a large number of potential agents are screened for ability to inhibit the activity. For proteins that interact with another protein or nucleic acid, binding assays are established to measure such interaction directly, and the potential agents are screened for ability to inhibit the binding interaction.

The use of different assays known in the art is contemplated according to this aspect of the invention. When the function of the virulence gene product is known or predicted by sequence similarity to a known gene product, potential inhibitors can be screened in enzymatic or other types of biological and/or biochemical assays keyed to the function and/or properties of the gene product. When the virulence gene product is known or predicted by sequence similarity to a known gene product to interact with another protein or nucleic acid, inhibitors of the interaction can be screened directly in binding assays. The invention contemplates a multitude of assays to screen and identify inhibitors of binding by the virulence gene product. In one example, the virulence gene product is immobilized and interaction with a binding partner is assessed in the presence and absence of a putative inhibitor compound. In another example, interaction between the virulence gene product and its binding partner is assessed in a solution assay, both in the presence and absence of a putative inhibitor compound. In both assays, an inhibitor is identified as a compound that decreases binding between the virulence gene product and its binding partner. Other assays are also contemplated in those instances wherein the virulence gene product binding partner is a protein. For example, variations of the di-hybrid assay are contemplated wherein an inhibitor of protein/protein interactions is identified by detection of a positive signal in a transformed or transfected host cell as described in PCT publication number WO 95/20652, published August 3, 1995.

Candidate inhibitors contemplated by the invention include compounds selected from libraries of potential inhibitors. There are a number of different libraries used for the identification of small molecule modulators, including: (1) chemical

libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules. Chemical libraries consist of structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening. Natural product libraries are collections of microorganisms, animals, plants, or marine organisms which are used to create mixtures for screening by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of plants or marine organisms. Natural product libraries include polyketides, non-ribosomal peptides, and variants (non-naturally occurring) thereof. For a review, see *Science 282*:63-68 (1998). Combinatorial libraries are composed of large numbers of peptides, oligonucleotides, or organic compounds as a mixture. They are relatively easy to prepare by traditional automated synthesis methods, PCR, cloning, or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol. 8*:701-707 (1997). Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to modulate activity.

Still other candidate inhibitors contemplated by the invention can be designed and include soluble forms of binding partners, as well as binding partners as chimeric, or fusion, proteins. Binding partners as used herein broadly encompasses antibodies, antibody fragments, and modified compounds comprising antibody domains that are immunospecific for the expression product of the identified virulence gene.

Other assays may be used when a binding partner (*i.e.,* ligand) for the virulence gene product is not known, including assays that identify binding partners of the target protein through measuring direct binding of test binding partner to the target protein, and assays that identify binding partners of target proteins through affinity ultrafiltration with ion spray mass spectroscopy/HPLC methods or other physical and analytical methods. Alternatively, such binding interactions are evaluated indirectly using the yeast two-hybrid system described in Fields and Song, *Nature, 340*:245-246

(1989), and Fields and Sternglanz, *Trends in Genetics, 10*:286-292 (1994), both of which are incorporated herein by reference. The two-hybrid system is a genetic assay for detecting interactions between two proteins or polypeptides. It can be used to identify proteins that bind to a known protein of interest, or to delineate domains or residues critical for an interaction. Variations on this methodology have been developed to clone genes that encode DNA-binding proteins, to identify peptides that bind to a protein, and to screen for drugs. The two-hybrid system exploits the ability of a pair of interacting proteins to bring a transcription activation domain into close proximity with a DNA-binding domain that binds to an upstream activation sequence (UAS) of a reporter gene, and is generally performed in yeast. The assay requires the construction of two hybrid genes encoding (1) a DNA-binding domain that is fused to a first protein and (2) an activation domain fused to a second protein. The DNA-binding domain targets the first hybrid protein to the UAS of the reporter gene; however, because most proteins lack an activation domain, this DNA-binding hybrid protein does not activate transcription of the reporter gene. The second hybrid protein, which contains the activation domain, cannot by itself activate expression of the reporter gene because it does not bind the UAS. However, when both hybrid proteins are present, the noncovalent interaction of the first and second proteins tethers the activation domain to the UAS, activating transcription of the reporter gene. When the virulence gene product (the first protein, for example) is already known to interact with another protein or nucleic acid, this assay can be used to detect agents that interfere with the binding interaction. Expression of the reporter gene is monitored as different test agents are added to the system; the presence of an inhibitory agent results in lack of a reporter signal.

When the function of the virulence gene product is unknown and no ligands are known to bind the gene product, the yeast two-hybrid assay can also be used to identify proteins that bind to the gene product. In an assay to identify proteins that bind to the first protein (the target protein), a large number of hybrid genes each encoding different second proteins are produced and screened in the assay. Typically, the second protein is encoded by a pool of plasmids in which total cDNA or genomic DNA is ligated to the activation domain. This system is applicable to a wide variety of proteins, and it is not even necessary to know the identity or function of the second binding protein. The

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system is highly sensitive and can detect interactions not revealed by other methods; even transient interactions may trigger transcription to produce a stable mRNA that can be repeatedly translated to yield the reporter protein.

Other assays may be used to search for agents that bind to the target protein. One such screening method to identify direct binding of test ligands to a target protein is described in U.S. Patent No. 5,585,277, incorporated herein by reference. This method relies on the principle that proteins generally exist as a mixture of folded and unfolded states, and continually alternate between the two states. When a test ligand binds to the folded form of a target protein (i.e., when the test ligand is a ligand of the target protein), the target protein molecule bound by the ligand remains in its folded state. Thus, the folded target protein is present to a greater extent in the presence of a test ligand which binds the target protein, than in the absence of a ligand. Binding of the ligand to the target protein can be determined by any method which distinguishes between the folded and unfolded states of the target protein. The function of the target protein need not be known in order for this assay to be performed. Virtually any agent can be assessed by this method as a test ligand, including, but not limited to, metals, polypeptides, proteins, lipids, polysaccharides, polynucleotides and small organic molecules.

Another method for identifying ligands for a target protein is described in Wieboldt *et al.*, *Anal. Chem.*, 69:1683-1691 (1997), incorporated herein by reference. This technique screens combinatorial libraries of 20-30 agents at a time in solution phase for binding to the target protein. Agents that bind to the target protein are separated from other library components by centrifugal ultrafiltration. The specifically selected molecules that are retained on the filter are subsequently liberated from the target protein and analyzed by HPLC and pneumatically assisted electrospray (ion spray) ionization mass spectroscopy. This procedure selects library components with the greatest affinity for the target protein, and is particularly useful for small molecule libraries.

The inhibitors/binders identified by the initial screens are evaluated for their effect on virulence in *in vivo* mouse models of *P. multocida* infections. Models of bacteremia, endocarditis, septic arthritis, soft tissue abscess, or pneumonia may be utilized. Models involving use of other animals are also comprehended by the invention.

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For example, rabbits can be challenged with a wild type *P. multocida* strain before or after administration of varying amounts of a putative inhibitor/binder compound. Control animals, administered only saline instead of putative inhibitor/binder compound provide a standard by which deterioration of the test animal can be determined. Other animal models include those described in the <u>Animal and Plant Health Inspection Sevice, USDA</u>, January 1, 1994 Edition, §§113.69-113.70; Panciera and Corstvet, *Am. J. Vet. Res. 45*:2532-2537; Ames, *et al., Can. J. Comp. Med. 49*:395-400 (1984); and Mukkur, *Infection and Immunity 18*:583-585 (1977). Inhibitors/binders that interfere with bacterial virulence are can prevent the establishment of an infection or reverse the outcome of an infection once it is established.

Any adjuvant known in the art may be used in the vaccine composition, including oil-based adjuvants such as Freund's Complete Adjuvant and Freund's Incomplete Adjuvant, mycolate-based adjuvants (*e.g.,* trehalose dimycolate), bacterial lipopolysaccharide (LPS), peptidoglycans (*i.e.,* mureins, mucopeptides, or glycoproteins such as N-Opaca, muramyl dipeptide [MDP], or MDP analogs), proteoglycans (*e.g.,* extracted from *Klebsiella pneumoniae*), streptococcal preparations (*e.g.,* OK432), Biostim™ (*e.g.,* 01K2), the "Iscoms" of EP 109 942, EP 180 564 and EP 231 039, aluminum hydroxide, saponin, DEAE-dextran, neutral oils (such as miglyol), vegetable oils (such as arachis oil), liposomes, Pluronic® polyols, the Ribi adjuvant system (see, for example GB-A-2 189 141), or interleukins, particularly those that stimulate cell mediated immunity. An alternative adjuvant consisting of extracts of *Amycolata*, a bacterial genus in the order Actinomycetales, has been described in U.S. Patent No. 4,877,612. Additionally, proprietary adjuvant mixtures are commercially available. The adjuvant used will depend, in part, on the recipient organism. The amount of adjuvant to administer will depend on the type and size of animal. Optimal dosages may be readily determined by routine methods.

The vaccine compositions optionally may include vaccine-compatible pharmaceutically acceptable (*i.e.,* sterile and non-toxic) liquid, semisolid, or solid diluents that serve as pharmaceutical vehicles, excipients, or media. Any diluent known in the art may be used. Exemplary diluents include, but are not limited to, polyoxyethylene sorbitan monolaurate, magnesium stearate, methyl- and

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propylhydroxybenzoate, talc, alginates, starches, lactose, sucrose, dextrose, sorbitol, mannitol, gum acacia, calcium phosphate, mineral oil, cocoa butter, and oil of theobroma.

The vaccine compositions can be packaged in forms convenient for delivery. The compositions can be enclosed within a capsule, caplet, sachet, cachet, gelatin, paper, or other container. These delivery forms are preferred when compatible with entry of the immunogenic composition into the recipient organism and, particularly, when the immunogenic composition is being delivered in unit dose form. The dosage units can be packaged, e.g., in tablets, capsules, suppositories or cachets.

The vaccine compositions may be introduced into the subject to be immunized by any conventional method including, e.g., by intravenous, intradermal, intramuscular, intramammary, intraperitoneal, or subcutaneous injection; by oral, sublingual, nasal, anal, or vaginal, delivery. The treatment may consist of a single dose or a plurality of doses over a period of time.

The invention also comprehends use of an attenuated bacterial strain of the invention for manufacture of a vaccine medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith. The invention also provides use of inhibitors of the invention for manufacture of a medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith.

The present invention is illustrated by the following examples. Example 1 describes constructions of *P. multocida* mutants. Example 2 relates to screening for *P. multocida* mutants. Example 3 addresses methods to determine virulence of the *P. multocida* mutants. Example 4 describes cloning of *P. multocida* virulence genes. Example 5 addresses identification of genes in other species related to *P. multocida* virulence genes. Example 6 describes construction of *A. pleuropneumoniae* mutants. Example 7 addresses screening for attenuated *A. pleuropneumoniae* mutants. Example 8 relates to identification of *A. pleuropneumoniae* virulence genes. Example 9 describes competition challenge of *A. pleuropneumoniae* mutants and wild type bacteria. Example 10 characterizes *A. pleuropneumoniae* genes identified. Example 11 addresses efficacy of *A. pleuropneumoniae* mutant to protect against wild type bacterial challenge.

Example 1
Construction of a Library of Tagged-Transposon *P. multocida* Mutants

A library of tagged-transposon mutants was constructed in parental vector pLOF/Km [Herrero, *et al., J Bacteriol. 172*:6557-67 (1990)] which has previously been demonstrated to be functional and random in *P. multocida* [Lee, *et al., Vet Microbiol. 50*:143-8 (1996)]. Plasmid pLOF/Km was constructed as a modification of suicide vector pGP704 and included a transposase gene under control of the *Tac* promoter as well as the mini-Tn10 transposable element encoding kanamycin resistance. Plasmid pTEF-1 was constructed as described below by modifying pLOF/Km to accept sequence tags which contained a semi-random [NK]$_{35}$ sequence.

Plasmid pLOF/Km was first modified to eliminate the unique *Kpn*I restriction site in the multiple cloning region and then to introduce a new *Kpn*I site in the mini-Tn10 region. The plasmid was digested with *Kpn*I and the resulting overhanging ends were filled in with Klenow polymerase according to manufacturer's suggested protocol. Restriction digests and ligations described herein were performed according to manufacturer's suggested protocols (Gibco BRL, Gaithersburg, MD and Boehringer Mannheim, Indianapolis, IN). The blunt end product was self-ligated to produce a plasmid designated pLOF/Km--*Kpn*I which was transformed into *E.coli* DH5α:λpir for amplification. *E.coli* DH5α: (λpir φ80dlacZΔM15, recA1, endA1, gyrA96, thi-1, hsdR17(r_k^-, m_k, supE44, relA1, deoR, Δ(lacZYA-argF)U169, was propagated at 37°C in Luria-Bertani (LB) medium. Plasmids were prepared using QIAGEN SpinPreps from QIAGEN Inc. (Santa Clarita, CA) and digested with *Sfi*I which cuts at a unique site within the mini-Tn10 transposable element. A *Sfi*I-*Kpn*I-*Sfi*I adaptor was prepared by annealing oligonucleotides TEF1 (SEQ ID NO: 86) and TEF3 (SEQ ID NO: 87) and the resulting double-stranded adapter was ligated into the *Sfi*I site to create plasmid pTEF-1. Oligonucleotides TEF1 and TEF3 (as well as all other oligonucleotides described herein) were synthesized by Genosys Biotechnologies (The Woodlands, TX).

TEF1   5′-AGGCCGGTACCGGCCGCCT   SEQ ID NO: 86

TEF3   5′-CGGCCGGTACCGGCCTAGG   SEQ ID NO: 87

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Unique sequence tags for insertion into the *Kpn*I site of pTEF-1 were prepared as follows. PCR was carried out to generate double stranded DNA tags using a GeneAmp XL PCR Kit (PE Applied Biosystems, Foster City, CA) under conditions including 250 μM each dNTP, 1.5 mM Mg(OAc)$_2$, 100 pmol each primer TEF14 (SEQ

5   ID NO: 88) and TEF15 (SEQ ID NO: 89), 1 ng TEF26 (SEQ ID NO: 90) as template DNA and 2.5 units recombinant *Tth* DNA Polymerase XL.

          TEF14   5′-CATGGTACCCATTCTAAC   SEQ ID NO: 88

10   TEF15   5′-CTAGGTACCTACAACCTC   SEQ ID NO: 89

          TEF26   SEQ ID NO: 90

    5′-CTAGGTACCTACAACCTCAAGCTT-[NK]$_{35}$-

                  AAGCTTGGTTAGAATGGGTACCATG

15   Reaction conditions included an initial incubation at 95°C for one minute, followed by thirty cycles of 30 seconds at 95°C, 45 seconds at 45°C, and 15 seconds at 72°C, followed by a final incubation at 72°C for two minutes. The PCR products were digested with *Kpn*I and purified using a QIAGEN Nucleotide Removal Kit (QIAGEN,

20   Inc., Chatsworth, GA) according to the manufacturer's suggested protocol. The unique tag sequences were ligated into the mini-Tn10 element of linearized pTEF-1, previously digested with *Kpn*I and dephosphorylated with calf intestinal alkaline phosphatase (Boehringer Mannheim) using standard procedures. The resulting plasmid library was transformed into *E.coli* DH5α:λpir. Colony blot analysis was performed according to

25   the DIG User's Guide (Boehringer-Mannheim) with hybridization and detection performed as follows.

        Hybridizations were essentially performed according to the Genius Non-Radioactive User's Guide (Boehringer Mannheim Biochemicals), the product sheet for the DIG-PCR labeling kit (Boehringer Mannheim Biochemicals), and the product sheet

30   for CSPD (Boehringer Mannheim Biochemicals). For preparation of probes, a 100 μl primary PCR reaction was set up using Amplitaq PCR buffer (PE Applied Biosystems),

200 μM dNTPs, 140 pmol each of primers TEF5 (SEQ ID NO: 91) and TEF6 (SEQ ID NO: 92), 2 mM MgCl₂, 2.5 units Amplitaq (PE Applied Biosystems) and 1 ng of plasmid DNA.

TEF5   5′-TACCTACAACCTCAAGCT   SEQ ID NO: 91

TEF6   5′-TACCCATTCTAACCAAGC   SEQ ID NO: 92

Cycle conditions included an initial incubation at 95°C for two minutes, followed by 35 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The amplification products were separated using electrophoresis on a 2% - 3:1 NuSieve GTG (FMC BioProducts, Rockland, ME, USA):Agarose gel and the 109 bp product was excised and purified. Gel extractions were carried out using a QIAGEN Gel Extraction kit (QIAGEN). Approximately 15 ng of the primary product was labeled in a 50 μl PCR reaction using the DIG PCR Kit, 50 pmol each of primers TEF24 and TEF25, and a 1:1 mix of DIG Probe Synthesis Mix with 2 mM dNTP stock solution.

TEF24   5′-TACCTACAACCTCAAGCTT   SEQ ID NO: 93

TEF25   5′-TACCCATTCTAACCAAGCTT   SEQ ID NO: 94

PCR conditions included an initial incubation at 95°C for four minutes, followed by 25 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The labeled PCR product was digested with HindIII in a total reaction volume of 90 μl and purified from the constant primer arms using a 2% - 3:1 NuSieve GTG (FMC BioProducts):Agarose gel. The region containing the labeled variable tag was excised and the entire gel slice was dissolved and denatured in 10 ml of DIG EasyHyb at 95°C for ten minutes.

Dot blots were prepared using a Hybond®-N⁺ membrane (Amersham-Pharmacia Biotech). Target DNA for each tag was prepared in 96 well plates using

approximately 30 ng of PCR product. An equal volume of 0.1 N NaOH was added to denature the sample and each sample was applied to the membrane with minimal vacuum using a Minifold I™ Dot-Blot Apparatus from Schleicher and Schuell (Keene, NH, USA). Each well was washed with 150 μl of Neutralization Solution (0.5 M Tris /3 M NaCl, pH 7.5) and 150 μl of 2X SSC. Membranes were UV-crosslinked in a Stratalinker (Stratagene, La Jolla, CA, USA) and prehybridized for one hour in 20 mls DIG EasyHyb Buffer at 42°C. The denatured probe was added and hybridization carried out overnight at 42°C. The membrane was washed two times in 2X SSC containing 0.1% SDS for five minutes each wash. Two high stringency washes were performed in 50 ml of pre-warmed 0.1X SSC buffer containing 0.1% SDS at 68°C for 15 minutes before proceeding with standard Genius Detection protocols (Genius Manual).

It is desirable to use a non-radioactive detection system for safety, lower cost, ease of use, and reduction of hazardous materials. In initial experiments using similar procedures previously described [Mei, *et al.*, *Mol Microbiol.* 26:399-407 (1997)], unacceptable background levels of hybridization were obtained in negative controls. In order to decrease background, tag length was increased by 30 bp to a total of 70, amplification primers were lengthened to include all sequence flanking the variable region, a lower concentration of dig-dUTP was used, and the conserved sequences flanking the sequence tag region were removed by gel purification. Most significantly, PCR was used to generate $[NK]_{35}$ sequence tags as the target DNA in dot blots rather than the entire plasmids containing the tagged transposons after detecting background hybridization from the transposon itself. Using these modifications background was eliminated making chemiluminescent/non-radioactive screening more effective.

Approximately four hundred different transformants resulting from the ligation of pTEF-1 with the PCR generated sequence tags were screened by colony blot and the 96 strongest hybridizing colonies were assembled into microtiter plates for further use. Even though the likelihood of duplicated tags was very low, half of the plate of master tags was probed against the other to confirm that no tags were duplicated. The plasmids containing these tags were purified and transformed into *E.coli* S17-1:λpir (pir, *recA, thi, pro, hsd,* (r-m+), RP4-2, (Tc::Mu), (Km::Tn7), [TmpR], [SmR]), and the transformed bacteria propagated at 37°C in Luria-Bertani (LB) medium. Each of the 96

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E.coli S17-1:λpir transformants containing the tagged plasmid pTEF-1 was used in conjugative matings to generate transposon mutants of *P. multocida*. *P. multocida* strain TF5 is a spontaneous nalidixic acid resistant mutant derived from UC6731, a bovine clinical isolate. *P. multocida* strains were grown on brain heart infusion (BHI) media (Difco Laboratories, Detroit, MI, USA) at 37°C and in 5% CO_2 when grown on plates. Matings were set up by growing each *E.coli* S17-1:λpir /pTEF1:[NK]$_{35}$ clone and the TF5 strain to late log phase. Fifty μl of culture for each tagged-pTEF-1 clone was mixed with 200 μl of the TF5 culture and 50 μl of each mating mixture was spotted onto 0.22 TM filters previously placed on BHI plates containing 100 mM IPTG and 10 mM $MgSO_4$. Following overnight incubation at 37°C with 5% CO_2, mating mixtures were washed off of each filter into 3 ml of PBS and 25 μl of each was plated onto BHIN^{50}K^{100} plates. Following selective overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 μl BHIN^{50}K^{50} making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50 μl of 75% glycerol was added to each well and plates were stored frozen at -80°C.

Nineteen pools were assembled by transferring the transposon mutants to microtiter plates making sure that each well contained a transposon mutant with the appropriate tag for that well. In other words, a specific well in each microtiter plate always contained a transposon mutant with the same sequence tag even though the location of the transposon within those mutants may be different.

Example 2
Murine Screening for Attenuated *P. multocida* Mutants

Nineteen pools of *Pasteurella multocida* transposon mutants were screened using a murine model of septicemia. Frozen plates of pooled *P. multocida* transposon mutants were removed from -80°C storage and subcultured by transferring 10 μl from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 200 μl of brain heart infusion (DIFCO) with 50 μg/ml nalidixic acid (Sigma) and 50 μg/ml kanamycin (Sigma) (BHIN^{50}K^{50}). Plates were incubated without shaking overnight at 37°C in 5% CO_2. Overnight plates were subcultured by transferring 10 μl from each well to a new flat bottomed 96-well plate (Corning Costar)

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containing 100 μl of BHI per well and incubating at 37°C with shaking at approximately 150 rpm. The OD_{540} was monitored using a micro-titer plate reader. At an OD_{540} of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100 μl from each of the wells of the micro-titer plate. The culture was diluted appropriately in BHI to doses of approximately 10^4, 10^5, 10^6 CFU/ml and 0.2 ml of each dilution was used to infect female 14-16 g BALB/c mice by intraperitoneal administration. At two days post-infection, one or two surviving mice were euthanized and the spleens harvested. The entire spleen was homogenized in 1.0 ml sterile 0.9 % saline. Dilutions of the homogenate from 10^{-2} to 10^{-5} were prepared and plated onto $BHIN^{50}K^{50}$ plates. Following overnight growth, at least 20,000 colonies were pooled in 10 mls BHI broth to form the "recovered pool" and 0.5 ml of the recovered pool was centrifuged at 3,500 X g and the pellet used to prepare genomic DNA according to a previously described protocol [Wilson, *In* F. M. Ausubel, *et al.,* (ed.), <u>Current Protocols in Molecular Biology</u>, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5. (1997)].

Initial experiments with virulent wild-type *P. multocida* indicated that organisms could be recovered from the spleen, lungs, kidneys, and liver indicating a truly septicemic model of infection. Dot blots for both the "input" and "recovered" pools were performed as described in Example 1 and evaluated both by visual inspection and by semi-quantitative analysis. Hybridization was carried out as described in Example 1 except that 5 μg of genomic DNA from input and recovered pools was used as template. Semi-quantitative analysis indicates whether a significant reduction in a single clone has occurred. If a mutant is unable to survive within the host, then the recovered signal should be very low compared to the input signal yielding a high input/recovered ratio. Most mutants will grow as well *in vivo* as *in vitro* and therefore a ratio of their signals should be approximately equal to 1. Clones selected by quantitative analysis as being highly reduced in the recovered pool were selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots.

Example 3
Determination of Virulence for *P. multocida* Candidate Mutants

Each potential mutant which exhibited reduced recovery from splenic tissue was isolated from the original pool plate and used individually in a challenge experiment to verify and roughly estimate the attenuation caused by the transposon mutation. Individual candidate mutants from *in vivo* screens were grown on Sheep Blood Agar plates overnight in 5% CO_2 at 37°C. Approximately six colonies of each mutant were inoculated into BHI broth and allowed to grow for six hours. Dilutions were prepared and five mice each were infected as described above with 10^2, 10^3, 10^4 and 10^5 CFU each. Attenuation was determined by comparing mortality after six days relative to the wild type. Surviving mice were presumed to be protected and then challenged with a dose of wild type *P. multocida* at a concentration approximately 200-fold greater than the LD_{50} for the wild type strain. Survival rate was then determined for each challenged group of mice.

Results indicated that 62 of 120 potential transposon mutants were attenuated, having an approximate LD_{50} of at least 10 fold higher than the wild type strain. The clones and their approximate LD_{50} values are listed in Table 1. A control experiment with the wild type strain was run in parallel with each set of challenges and in all cases mortality in wild type-challenged groups was 100%.

In addition to LD_{50} values, Table 1 also provides data from vaccination and challenge experiments. Briefly, groups of mice (n = 5 to 10) were vaccinated by intraperitoneal injection with the individual *P. multocida* strains shown in Table 1 at a dose that was approximately 200 times greater than the LD_{50} of the virulent, wild type strain. Animals were observed for 28 days after which mortality figures were calculated.

Table 1
P. multocida Virulence Genes

Nucleotide SEQ ID NO:	Representative Isolate	PossibleGene Function	Vaccination # survivors/total	Challenge # survivors/total	LD_{50}
--	wild type	-	0/10	-	<10
23	PM1B1	guaB	10/10, 10/10, 10/10	9/10, 9/10	4.3 x 106
11	PM1D1	dsbB	10/10, 5/10	10/10, 5/5	8.4 x 104
3	PM1BD7	atpG	5/5, 10/10	10/10	>3 x 105
74	PM1BE11	yhcJ (HI0145)	10/10	5/10	>2 x 105
70	PM1BF6	yabK (HI1020)	3/5, 8/10	9/9	>2 x 105
19	PM2G8	fhaC	4/5, 9/10	9/9	>4 x 105

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Nucleotide SEQ ID NO:	Representative Isolate	PossibleGene Function	Vaccination # survivors/total	Challenge # survivors/total	LD$_{50}$
76	PM3C9	yiaO (HI0146)	3/5		>6 x 105
118	PM3G11	UnkO	4/5, 10/10	10/10	>3 x 105
31	PM7B4	iroA (UnkB)	0/5		
17	PM4C6	fhaB (fhaB2)	2/5, 10/10, 9/10	10/10, 9/9	>3 x 106
9	PM4G10-T9	dnaA	4/5		>5 x 105
1	PM4D5-T5	atpB	5/5		>4 x 105
53	PM4D5-T1	UnkC2	5/5		>4 x 105
15	PM4F2	fhaB (fhaB1)	3/5, 6/10, 10/10	6/6, 10/10	>3 x 105
41	PM5F7	mreB	4/5		1 x 103
7	PM5E2	devB	0/5, 3/10	2/3	?
68	PM6H5-T1	xylA	5/5		>3 x 105
78	PM6H8	yigF (HI0719)	5/5, 9/10	9/9	>3 x 105
108	PM7D12	pnp	5/5, 9/10	9/9	
51	PM8C1R1-T2	UnkC1	5/5		~6 x 105
37	PM8C1-T3	mglB	5/5		~6 x 105
58	PM8C1R1-T6	UnkD1	5/5		~6 x 105
45	PM10H7	purF (HI1207)	3/5, 8/10, 8/10	8/8, 8/8	>3 x 105
25	PM10H10-T2	HI1501	5/5		>1 x 104
72	PM11G8-T2	ygiK	5/5		>2.4 x 103
21	PM11G8-T4	greA	5/5		>2.4 x 103
84	PM12H6	yyam (HI0687)	3/5, 0/10		~2.2 x 103
33	PM15G8-T2	kdtB	5/5		>1.2 x 105
116	PM15G8-T1	UnkK	5/5		>1.2 x 105
104	PM16G11-T1	hmbR	3/5		>1.9 x 105
29	PM16G11-T2	hxuC	3/5		>1.9 x 105
35	PM16H8	lgtC	5/5, 10/10	10/10	>2.4 x 105
80	PM16H3	yleA (HI0019)	5/5, 10/10		> 2.0 x 105
49	PM17H6-T1	sopE	4/5		~6 x 105
120	PM17H6	UnkP	4/5		~6 x 105
5	PM18F5-T8	cap5E	5/5		>2.4 x 105
82	PM18F5-T10	yojB (HI0345)	5/5		>2.4 x 105
13	PM19A1	exbB	5/5, 10/10	10/10	>1.2 x 105
112	PM19D4	rci	5/5, 8/10	8/8	~1.6 x 105
39	PM20A12	mioC (HI0669)	3/5, 8/10	8/8	~2 x 104
60	PM20C2	UnkD2	5/5, 10/10	10/10	>8.2 x 106

Example 4
Cloning and Identification of Genes Required for *P. multocida* Virulence

Each transposon mutant which was verified to be attenuated was analyzed further to determine the identity of the disrupted open reading frame. DNA from each mutant was amplified, purified, and digested with restriction enzymes that were known not to cut within the transposon and generally produced 4-8 kb fragments that hybridized with the transposon. Using selection for kanamycin resistance encoded by the transposon, at least one fragment for each transposon mutant was cloned.

Southern hybridization with multiple restriction enzymes was performed for each attenuated mutant using a labeled 1.8 kb *Mlu*I fragment from pLOF/Km as a probe to identify a suitably sized fragment for cloning. The mini-Tn10 element and

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flanking DNA from each mutant was cloned into pUC19 and the flanking sequence determined using internal primers TEF32 and TEF40, primer walking and in some cases universal pUC-19 primers.

TEF-32   GGCAGAGCATTACGCTGAC   SEQ ID NO: 95

TEF-40   GTACCGGCCAGGCGGCCACGCGTATTC   SEQ ID NO:96

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Double stranded sequence for putative interrupted open reading frames was obtained for each clone. Sequencer 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs [Devereux, *et al.,* 1997. Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer Group, Inc., Madison] were used to search for homologous sequences in currently available databases.

In 37% of the clones that were identified as being attenuated, there were multiple insertions of the mini-Tn10 transposable element. Each insertion including its flanking sequence was cloned individually into pGP704 and mated into the wild-type strain to produce new mutants of *P. multocida*, each carrying only one of the multiple original insertions. Individual mutants were retested individually to determine the insertion responsible for the attenuated phenotype. The nucleotide sequence of the disrupted, predicted open reading frame was determined by sequencing both strands, and the predicted amino acid sequence was used to search currently available databases for similar sequences. Sequences either matched known genes, unknown genes, and hypothetical open reading frames previously sequenced or did not match any previously identified sequence. For those genes having homology to previously identified sequences, potential functions were assigned as set out in Table 1.

Example 5
Identification of Related Genes in Other Species

In separate experiments, STM was also performed using *Actinobacillus pleuropneumoniae* (App). One of the App strains contained an insertion in a gene that was sequenced (SEQ ID NO: 97) and identified as a species homolog of the *P. multocida*

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atpG gene. This result suggested the presence in other bacterial species of homologs to previously unknown *P. multocida* genes that can also be mutated to produce attenuated strains of the other bacterial species for use in vaccine compositions. In order to determine if homologs of other *P. multocida* genes exists in other bacterial species, Southern hybridization was performed on genomic DNA from other species using the *A. pleuropneumoniae atpG* gene as a probe.

Actinobacillus pleuropneumoniae, Pasteurella haemolytica (Ph), *P. multocida*, and *Haemophilus somnus* (Hs) genomic DNA was isolated using the CTAB method and digested with *Eco*RI and *Hin*dIII for two hours at 37°C. Digested DNA was separated on a 0.7% agarose gel at 40V in TAE buffer overnight. The gel was immersed sequentially in 0.1 M HCL for 30 minutes, twice in 0.5 M NaOH/1.5 M NaCl for 15 minutes each, and twice in 2.5 M NaCl/1 M Tris, pH 7.5. The DNA was transferred to nitrocellulose membranes (Amersham Hybond N$^+$) overnight using 20X SSC buffer (3 M NaCl/0.3 M sodium citrate). The DNA was crosslinked to the membrane using a UV Stratalinker on autocrosslink setting (120 millijoules). The membrane was prehybridized in 5X SSC/ 1% blocking solution/0.1% sodium lauroyl sarcosine/0.02% SDS at 50°C for approximately seven hours and hybridized overnight at 50°C in the same solution containing a PCR generated atgG probe.

The probe was prepared using primers DEL-1389 (SEQ ID NO: 98) and TEF-46 (SEQ ID NO: 99) in a with a GeneAmp XL PCR kit in a GeneAmp PCR System 2400. Template was genomic *A. pleuropneumoniae* DNA.

DEL-1389	TCTCCATTCCCTTGCTGCGGCAGGG	SEQ ID NO: 98
TEF-46	GGAATTACAGCCGGATCCGGG	SEQ ID NO: 99

The PCR was performed with an initial heating step at 94°C for five minutes, 30 cycles of denaturation t 94°C for 30 sec, annealing at 50°C for 30 sec, and elongation at 72°C for three minutes, and a final extension step at 72°C for five minutes. The amplification products were separated on an agarose gel, purified using a QIAquick gel purification kit (QIAGEN), and labeled using a DIG-High Primer kit (Boehringer Mannheim). The blot was removed from the hybridization solution and rinsed in 2X SSC and washed two times for five minutes each wash in the same buffer. The blot was then washed two

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times for 15 minutes each in 0.5X SSC at 60°C. Homologous bands were visualized using a DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

Single bands were detected in *Pasteurella haemolytica*, *Haemophilus somnus* and *A. pleuropneumoniae* using *Eco*RI digested DNA. Two bands were detected using *Eco*Ri digested DNA from *Pasteurella multocida*.

Example 6
Construction of a Library of Tagged-Transposon *P. multocida* Mutants

Transposon mutagenesis using pLOF/Km has previously been reported to be functional and random in *A. pleuropneumoniae* [Tascon, *et al.*, *J Bacteriol.* *175*:5717-22 (1993)]. To construct tagged transposon mutants of *A. pleuropneumoniae*, each of 96 *E. coli* S17-1:λpir transformants containing pre-selected tagged plasmids (pTEF-1:[NK]$_{35}$) was used in conjugative matings to generate transposon mutants of *A. pleuropneumoniae* strain AP225, a serotype 1 spontaneous nalidixic acid resistant mutant derived from an in vivo passaged ATCC 27088 strain. *A. pleuropneumoniae* strains were grown on Brain Heart Infusion (BHI) (Difco Laboratories, Detroit, MI) media with 10 μg/ml B-nicotinamide adenine dinucleotide (V^{10}), (Sigma, St. Louis, Missouri) at 37°C and in 5% CO_2 when grown on plates. *E.coli* S17-1:λpir (λpir, *recA*, *thi*, *pro*, *hsdR*(r_k-,m_k+), RP4-2, (Tc^R::Mu), (Km^R::Tn7), [Tmp^R], [Sm^R]) was propagated at 37°C in Luria-Bertani (LB) medium. Antibiotics when necessary were used at 100 μg/ml ampicillin (Sigma), 50 μg/ml nalidixic acid (N^{50})(Sigma), and 50 (K^{50}) or 100 (K^{100}) μg/ml of kanamycin (Sigma).

Matings were set up by growing each *E. coli* S17-1:λpir/pTEF1:[NK]$_{35}$ clone and the AP225 strain to late log phase. A 50 μl aliquot of culture for each tagged-pTEF-1 clone was mixed with 150 μl of the APP225 culture, and then 50 μl of each mating mixture was spotted onto 0.22 μM filters previously placed onto $BHIV^{10}$ plates containing 100 μM IPTG and 10 mM $MgSO_4$. Following overnight incubation at 37°C with 5% CO_2, mating mixtures were washed off of each filter into 2 ml of PBS and 200 μl of each was plated onto $BHIV^{10}N^{50}K^{100}$ plates. After selective overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 μl $BHIV^{10}N^{50}K^{50}$ making sure that each well in a microtiter plate always contained a

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transposon mutant with the same sequence tag. Following overnight growth, 50 µl of 75% glycerol was added to each well and plates were stored frozen at -80°C.

APP does not appear to have as much bias towards multiple insertions of the mini-Tn10 element as did P. multocida. Only approximately 3% of the mutants were determined to contain multiple insertions, which is in agreement with the 4% previously reported [Tascon, et al., J Bacteriol. 175:5717-22 (1993)]. A problem in APP consisted of identifying numerous mutants (discussed below) containing insertions into 23S RNA regions: 28 total mutants with insertions into 13 unique sites. This may indicate that 23S RNA contains preferential insertion sites and that the growth of APP is affected by these insertions enough to result in differential survival within the host. Southern blot analysis using an APP 23S RNA probe suggests that APP may contain only three ribosomal operons as compared to five in H. influenzae [Fleischmann, et al., Science 269:496-512 (1995)] and seven complete operons in E. coli [Blattner, et al., Science 277:1453-1474 (1997)]. This site preference and its effect on growth rate may be a significant barrier to "saturation mutagenesis" since a significant number of clones will contain insertions into these rRNAs and large volume screening will be necessary to obtain additional unique attenuating mutations.

Example 7
Porcine Screening for Attenuated *A. pleuropneumoniae* Mutants

Twenty pools of *A. pleuropneumoniae* transposon mutants, containing a total of approximately 800 mutants, were screened using a porcine intratracheal infection model. Each pool was screened in two separate animals.

Frozen plates of pooled *A. pleuropneumoniae* transposon mutants were removed from -80°C storage and subcultured by transferring 20 µl from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 180 µl of $BHIV^{10}N^{50}K^{50}$. Plates were incubated without shaking overnight at 37°C in 5% CO_2. Overnight plates were then subcultured by transferring 10 µl from each well to a new flat bottomed 96 well plate (Corning Costar) containing 100 µl of $BHIV^{10}$ per well and incubating at 37°C with shaking at 150 rpm. The OD_{562} was monitored using a microtiter plate reader. At an OD_{562} of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100 µl from each of the wells of the microtiter

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plate. The culture was diluted appropriately in BHI to approximately 2 X 10^6 CFU/ml. For each diluted pool, 4.0 ml was used to infect 10-20 kg SPF pigs (Whiteshire-Hamroc, Albion, IN) by intratracheal administration using a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and the lungs removed. Lavage was performed to recover surviving bacteria by infusing 150 mls of sterile PBS into the lungs, which were then massaged to distribute the fluid. The lavage fluid was recovered, and the process was repeated a second time. The lavage fluid was centrifuged at 450 x g for 10 minutes to separate out large debris. Supernatants were then centrifuged at 2,800 x g to pellet the bacteria. Pellets were resuspended in 5 mls BHI and plated in dilutions ranging from 10^{-2} to 10^{-5} onto BHIV^{10}N^{50}K^{50} plates. Following overnight growth, at least 100,000 colonies were pooled in 10 mls BHI broth to form the "recovered pools". A 0.7 ml portion of each recovered pool was used to prepare genomic DNA by the CTAB method [Wilson, *In* Ausubel, *et al.*, (eds.), Current Protocols in Molecular Biology, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5 (1997)].

Recovery from the animals routinely was in the 10^8 CFU range from lung lavage.

Dot blots were performed and evaluated both by visual inspection and by semi-quantitative analysis as described previously. All hybridizations and detections were performed as described. Briefly, probes were prepared by a primary PCR amplification, followed by agarose gel purification of the desired product and secondary PCR amplification incorporating dig-dUTP. Oligonucleotides including TEF5, TEF6, TEF24, TEF25, TEF48 and TEF62, were synthesized by Genosys Biotechnologies (The Woodlands, TX). Primers TEF69, TEF65, and TEF66 were also used for inverse PCR reactions and sequencing.

TEF69	GACGTTTCCCGTTGAATATGGCTC	SEQ ID NO: 166
TEF65	GCCGGATCCGGGATCATATGACAAGA	SEQ ID NO: 167
TEF66	GACAAGATGTGTATCCACCTTAAC	SEQ ID NO: 168

The labeled PCR product was then digested with *Hin*dIII to separate the constant primer arms from the unique tag region. The region containing the labeled variable tag was excised and the entire gel slice was then dissolved and denatured in DIG

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EasyHyb. Dot blots were prepared and detected using the standard CSPD detection protocol. Film exposures were made for visual evaluation, and luminescent counts per second (LCPS) were determined for each dot blot sample. The $LCPS_{input}$ / $LCPS_{recovered}$ ratio for each mutant was used to determine mutants likely to be attenuated.

5   Clones selected as being present in the input pool but highly reduced in the recovered pool were selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots. A total of 110 clones were selected.

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Example 8
Identification of *A. pleuropneumoniae* Virulence Genes

A partial flanking sequence was determined for each of the 110 mutants by inverse PCR and direct product sequencing. Inverse PCR was used to generate flanking DNA products for direct sequencing as described above. Sequencing reactions

15 were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Sequencher 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs [Devereux and Haeberli, Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer Group, Inc., Madison (1997)] were used to

20 search for homologous sequences in currently available databases.

Table 2 shows the *A. pleuropneumoniae* genes identified and extent to which open reading frames were determinable. Sequence identification numbers are provided for nucleotide sequences as well as deduced amino acid sequences where located.

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Table 2
A. pleuropneumoniae Open Reading Frames

Complete Open Reading Frame		NO Start Codon - Stop Codon	
atpH	SEQ ID NO: 134	dksA	SEQ ID NO: 136
aptG	SEQ ID NO: 132	dnaK	SEQ ID NO: 138
exbB	SEQ ID NO: 140	HI0379	SEQ ID NO: 144
OmpP5	SEQ ID NO: 152		
OmpP5-2	SEQ ID NO: 150	NO Start Codon - NO Stop Codon	
tig	SEQ ID NO: 160	pnp	SEQ ID NO: 154
fkpA	SEQ ID NO: 142	apvA-or 1	SEQ ID NO: 122
hupA	SEQ ID NO: 146	apvA-or 2	SEQ ID NO: 124
rpmF	SEQ ID NO: 158	apvB	SEQ ID NO: 126
		apvD	SEQ ID NO: 130
Start Codon - NO Stop Codon			
lpdA	SEQ ID NO: 148	RNA or Noncoding Sequences	
potD	SEQ ID NO: 156	tRNA-leu	SEQ ID NO: 162
yaeE	SEQ ID NO: 164	tRNA-glu	SEQ ID NO: 163
apvC	SEQ ID NO: 128		

The putative identities listed in Table 3 (below, Example 9) were assigned by comparison with bacterial databases. The 110 mutants represented 35 groups of unique transposon insertions. The number of different mutations per loci varied, with some clones always containing an insertion at a single site within an ORF to clones containing insertions within different sites of the same ORF. Three multiple insertions were detected in the 110 mutants screened as determined by production of multiple PCR bands and generation of multiple sequence electropherograms.

Example 9
Competition Challenge of *A. pleuropneumoniae* Mutants with Wild Type APP225

A representative clone from each of the unique attenuated mutant groups identified above that was absent or highly reduced in the recovered population was isolated from the original pool plate and used in a competition challenge experiment with the wild type strain (AP225) to verify the relative attenuation caused by the transposon mutation. Mutant and wild type strains were grown in BHIV[10] to an OD_{590} of 0.6 – 0.9. Approximately 5.0 x 10^6 CFU each of the wild type and mutant strains were added to 4 mls BHI. The total 4 ml dose was used infect a 10-20 kg SPF pig by intratracheal

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administration with a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and the lungs removed. Lung lavages were performed as described above. Plate counts were carried out on $BHIV^{10}N^{50}$ and $BHIV^{10}N^{50}K^{100}$ to determine the relative numbers of wild type to mutant in both the input cultures and in the lung lavage samples. A Competitive Index (CI) was calculated as the [mutant CFU / wild type CFU]$_{input}$ / [mutant CFU / wild type CFU]$_{recovered}$.

Of the 35 potential transposon mutants, 22 were significantly attenuated, having a competitive index (CI) of less than 0.2. A transposon mutant that did not seem to be attenuated based on the STM screening results was chosen from one of the pools as a positive control. This mutant had a CI in vivo of approximately 0.6. An in vitro competition was also done for this mutant resulting in a CI of 0.8. The mutant was subsequently determined to contain an insertion between 2 phenylalanine tRNA's.

Competitive indices for unique attenuated single-insertion mutants are listed in Table 3. Competitive indices for *atpG*, *pnp*, and *exbB* App mutants indicated that the mutants were unable to compete effectively with the wild type strains and were therefore attenuated.

Table 3
Virulence and Proposed Function of *A. pleuropneumoniae* Mutants

Mutant	Similarity	Putative or Known Functions	C.I.
AP20A6	*atpH*	ATP synthase	.009
AP7F10	*atpG*	ATP synthase	.013
AP17C6	*lpdA*	dihydrolipoamide dehydrogenase	.039
AP11E7	exbB	transport of iron compounds	.003,.003,.006
AP3H7	*potD*	Spermidine/putrescine transport	.308
AP8H6	*OmpP5*	Adhesin / OmpA homolog	.184
AP18H8	*OmpP5-2*	Adhesin / OmpA homolog	.552
AP13E9	*tig*	Peptidyl-prolyl isomerase	.050
AP13C2	*fkpA*	Peptidyl-prolyl isomerase	<.001
AP15C11	*pnp*	Polynucleotide phosphorylase	.032
AP18F12	*hupA*	Histone – like protein	.001
AP20F8	*dksA*	Dosage dependent suppressor of dnaK mutations	.075
AP5G4	*dnaK*	Heat shock protein – molecular chaperone	.376

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AP17C9	*tRNA-leu*	Protein Synthesis (gene regulation?)	.059
AP5D6	*tRNA-glu*	Protein Synthesis	.055
AP18B2	*rpmF*	Protein Synthesis	.112
AP10E7	*yaeA*	Unknown	.001
AP19A5	HI0379	Unknown	.061
AP10C10	*apvA*	Unknown	.157
AP18F5	*apvB*	Unknown	.103
AP2A6	*apvC*	Unknown	.091
AP2C11	*apvD*	Unknown	.014

Accuracy of the CI appeared to be very good as the *exbB* mutant was competed within three different animals yielding CI's of 0.003, 0.003 and 0.006. The use of a Competitive Index number to assign attenuation based upon one competition in a large animal study was further confirmed based on preliminary vaccination results in pigs with 7 mutants (n=8) described below in Example 11.

Example 10
Characterization of Attenuated *A. pleuropneumoniae* Virulence Genes

The *A. pleuropneumoniae* genes identified represent four broad functional classes: biosynthetic enzymes, cellular transport components, cellular regulation components and unknowns.

The *atpG* gene, encoding the F1-γ subunit of the F_0F_1 H+-ATPase complex, can function in production of ATP or in the transport of protons by hydrolyzing ATP. A related *atpG* attenuated mutant was also identified in *P. multocida*. Another *atp* gene, *atpH*, that encodes the F_1 δ subunit was also identified. Phenotypes of *atp* mutants include non-adaptable acid-sensitivity phenotype [Foster, *J Bacteriol. 173*:6896-6902 (1991)], loss of virulence in *Salmonella typhimurium* [Garcia del Portillo, *et al., Infect Immun. 61*:4489-4492 (1993)] and *P. multocida* (above) and a reduction in both transformation frequencies and induction of competence regulatory genes in *Haemophilus influenzae* Rd [Gwinn, *et al., J Bacteriol. 179*:7315-20 (1997)].

LpdA is a dihydrolipoamide dehydrogenase that is a component of two enzymatic complexes: pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase.

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While the relationship to virulence is unknown, production of LpdA is induced in *Salmonella typhimurium* when exposed to a bactericidal protein from human which may suggest that this induction may be involved in attempts to repair the outer membrane [Qi, *et al., Mol Microbiol. 17*:523-31 (1995)].

Transport of scarce compounds necessary for growth and survival are critical in vivo. ExbB is a part of the TonB transport complex [Hantke, and Zimmerman, *Microbiology Letters. 49*:31-35 (1981)], interacting with TonB in at least two distinct ways [Karlsson, *et al., Mol Microbiol. 8*:389-96 (1993), Karlsson, *et al., Mol Microbiol. 8*:379-88 (1993)]. Iron acquisition is essential for pathogens. In this work, attenuated *exbB* mutants in both APP and *P. multocida* have been identified. Several TonB-dependent iron receptors have been identified in other bacteria [Biswas, *et al., Mol. Microbiol. 24*:169-179 (1997), Braun, *FEMS Microbiol Rev. 16*:295-307 (1995), Elkins, *et al., Infect Immun. 66*:151-160 (1998), Occhino, *et al., Mol Microbiol. 29*:1493-507 (1998),Stojiljkovic and Srinivasan, *J Bacteriol. 179*:805-12 (1997)]. *A. pleuropneumoniae* produces 2 transferrin-binding proteins, which likely depend on the ExbB/ExbD/TonB system, for acquisition of iron. PotD is a periplasmic binding protein that is required for spermidine (a polyamine) transport [Kashiwagi, *et al., J Biol Chem. 268*:19358-63 (1993)]. Another member of the *Pasteurellaceae* family, *Pasteurella haemolytica*, contains a homologue of *potD* (Lpp38) that is a major immunogen in convalescent or outer membrane protein vaccinated calves [Pandher and Murphy, *Vet Microbiol. 51*:331-41 (1996)]. In *P. haemolytica*, PotD appeared to be associated with both the inner and outer membranes. The role of PotD in virulence or in relationship to protective antibodies is unknown although previous work has shown *potD* mutants of *Streptococcus pneumoniae* to be attenuated [Polissi, *et al., Infect. Immun. 66*:5620-9 (1998)].

Relatively few "classical virulence factors," such as adhesins or toxins with the exception of homologues to OMP P5 of *Haemophilus influenzae*, were identified. *H. influenzae* OMP P5 is a major outer membrane protein that is related to the OmpA porin family of proteins [Munson, *et al., M Infect Immun. 61*:4017-20 (1993)]. OMP P5 in nontypeable *Haemophilus influenzae* has been shown to encode a fimbrial subunit protein expressed as a filamentous structure [Sirakova, *et al., Infect Immun.*

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62:2002-20 (1994)] that contributes to virulence and binding of both mucin and epithelial cells [Miyamoto and Bakaletz, *Microb Pathog. 21*:343-56 (1996), Reddy, *et al., Infect Immun. 64*:1477-9 (1996), Sirakova, *et al., Infect Immun. 62*:2002-20 (1994)]. A significant finding was identification of two distinct ORF's that appear to encode OMP P5 homologues. This is also the case with two very similar proteins, MOMP and OmpA2 from *Haemophilus ducreyi*. It remains to be determined whether both are functionally involved in the production of fimbriae and whether the presence of two such ORFs represents a divergent duplication with redundant or complementing functions. Interestingly, the two OMP P5 mutants seem to have disparate CI values, suggesting a difference in essentiality or functionality for only one copy. OMP P5 has been shown to undergo molecular variation during chronic infections [Duim, *et al., Infect Immun. 65*:1351-1356 (1997)], however, this appears to be restricted to a single gene undergoing point mutations resulting in amino acid changes rather than "type switching" due to differential expression of multiple genes.

Protein folding enzymes are important accessories for the efficient folding of periplasmic and extracellular proteins, and two genes were identified whose products have peptidyl-prolyl isomerase activity: *fkpA* and *tig* (trigger factor). FkpA is a periplasmic protein that is a member of the FK506-binding protein family [Horne and Young, *Arch Microbiol. 163*:357-65 (1995); Missiakas, *et al., Mol Microbiol. 21*:871-84 (1996)]. FkpA has been shown to contribute to intracellular survival of *Salmonella typhimurium* [Horne, *et al., Infect Immun. 65*:806-10 (1997)] and a *Legionella pneumophila* homolog, *mip* [Engleberg, *et al., Infect Immun. 57*:1263-1270 (1989)], is responsible for virulence and infection of macrophages [Cianciotto, *et al., J. Infect. Dis. 162*:121-6 (1990); Cianciotto, *et al., Infect. Immun. 57*:1255-1262 (1989)]. Tig, or trigger factor [Crooke and Wickner, *Proc. Natl. Acad. Sci. USA. 84*:5216-20 (1987), Guthrie, and Wickner, *J Bacteriol. 172*:5555-62 (1990), reviewed in Hesterkamp, and Bukau., *FEBS Lett. 389*:32-4 (1996)], is a peptidyl prolyl isomerase containing a typical FKBP region [Callebaut and Mornon, *FEBS Lett. 374*:211-215 (1995)], but is unaffected by FK506 [Stoller, *et al., EMBO J. 14*:4939-48 (1995)]. Tig has been shown to associate with the ribosomes and nascent polypeptide chains [Hesterkamp, *et al., Proc Natl Acad Sci USA 93*:4437-41 (1996), Stoller, *et al., EMBO J. 14*:4939-48 (1995)]. Possible roles

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include an unknown influence on cell division [Guthrie, and Wickner, *J Bacteriol.* *172*:5555-62 (1990)] in *E. coli*, a role in the secretion and activation of the *Streptococcus pyogenes* cysteine proteinase [Lyon, *et al., EMBO J. 17*:6263-75 (1998)] and survival under starvation conditions in *Bacillus subtilis* [Gothel, *et al., Biochemistry 37*:13392-9 (1998)].

Bacterial pathogens employ many mechanisms to coordinately regulate gene expression in order to survive a wide variety of environmental conditions within the host. Differences in mRNA stability can modulate gene expression in prokaryotes [Belasco and Higgins, *Gene 72*:15-23 (1988)]. For example, *rnr* (*vacB*) is required for expression of plasmid borne virulence genes in *Shigella flexneri* [Tobe, *et al., J Bacteriol. 174*:6359-67 (1992)] and encodes the RnaseR ribonuclease [Cheng, *et al., J. Biol. Chem. 273*:14077-14080 (1998)]. PNP is a polynucleotide phosphorylase that is involved in the degradation of mRNA. Null *pnp* / *rnr* mutants are lethal, suggesting a probable overlap of function. It therefore is possible that both *rnr* and *pnp* are involved in the regulation of virulence gene expression. A *pnp* mutant of *P. multocida* is avirulent in a mouse septicemic model (Example 2)]. Other *pnp*-associated phenotypes include competence deficiency and cold sensitivity in *Bacillus subtilis* [Wang and Bechhofer, *J Bacteriol. 178*:2375-82 (1996)].

HupA is a bacterial histone-like protein, which in combination with HupB constitute the HU protein in E. coli. Reports have suggested that *hupA* and *hupB* single mutants do not demonstrate any observable phenotype [Huisman, *et al., J Bacteriol. 171*:3704-12 (1989), Wada, *et al., J Mol Biol. 204*:581-91 (1988)], however, *hupA-hupB* double mutants have been shown to be cold sensitive, sensitive to heat shock and blocked in many forms of site-specific DNA recombination [Wada, *et al., J Mol Biol. 204*:581-91 (1988), Wada, *et al., Gene. 76*:345-52 (1989)]. One limited data previously indicated that *hupA* is directly involved in virulence [Turner, *et al., Infect Immun. 66*:2099-106 (1998)]. The mechanism of *hupA* attenuation remains unknown.

DnaK is a well known and highly conserved heat shock protein involved in regulatory responses to various stressful environmental changes [reviewed in Lindquist and Craig, *Annu Rev Genet. 22*:631-77 (1988)]. DnaK is also one of the most significantly induced stress proteins in *Yersinia enterocolitica* after being phagocytosed

by macrophages [Yamamoto, *et al., Microbiol Immunol. 38*:295-300 (1994)] and a *Brucella suis dnaK* mutant failed to multiply within human macrophage-like cells [Kohler, *et al., Mol Microbiol. 20*:701-12 (1996)]. In contrast, another intracellular pathogen, *Listeria monocytogenes*, did not show induction of *dnaK* after phagocytosis [Hanawa, *et al., Infect Immun. 63*:4595-9 (1995)]. A *dnaK* mutant of *Vibrio cholera* affected the production of ToxR and its regulated virulence factors in vitro but similar results were not obtained from in vivo grown cells [Chakrabarti, *et al., Infect Immun. 67*:1025-1033 (1999)]. The CI of *A. pleuropneumonia dnaK* mutant was higher than most of the attenuated mutants although still approximately half of the positive control strain.

DksA is a dosage dependent suppressor of filamentous and temperature-sensitive growth in a *dnaK* mutant of *E. coli* [Kang and Craig, *J Bacteriol. 172*:2055-64 (1990)]. There is currently no defined molecular function for DksA, but the gene has been identified as being critical for the virulence of *Salmonella typhimurium* in chickens and newly hatched chicks [Turner, *et al., Infect Immun. 66*:2099-106 (1998)]. In that work, it was noted that the *dksA* mutant did not grow well with glucose or histidine but did grow well with glutamine or glutamate as the sole carbon source. This observation may indicate that the *dksA* mutant is somehow impaired in the biosynthesis of glutamate [Turner, *et al., Infect Immun. 66*:2099-106 (1998)].

Three genes were identified that have roles in protein synthesis: tRNA-leu, tRNA-*glu* and *rpmF*. Excluding protein synthesis, tRNA's also have a wide variety of functional roles in peptidoglycan synthesis [Stewart, *et al., Nature 230*:36-38 (1971)], porphyrin ring synthesis [Jahn, *et al., Trends Biochem Sci. 17*:215-8 (1992)], targeting of proteins for degradation [Tobias, *et al., Science 254*:1374-7 (1991)], post-translational addition of amino acids to proteins [Leibowitz and Soffer, *B.B.R.C. 36*:47-53 (1969)] and mediation of bacterial-eukaryotic interactions [Gray, *et al., J Bacteriol. 174*:1086-98 (1992), Hromockyj, *et al., Mol Microbiol. 6*:2113-24 (1992)]. More specifically, tRNA-leu is implicated in transcription attenuation [Carter, *et al., Proc. Natl. Acad. Sci. USA 83*:8127-8131 (1986)], lesion formation by *Pseudomonas syringae* [Rich and Willis, J Bacteriol. 179:2247-58 (1997)] and virulence of uropathogenic *E. coli* [Dobrindt, *et al., FEMS Microbiol Lett. 162*:135-141 (1998), Ritter, *et al., Mol Microbiol. 17*:109-21

(1995)]. It is unknown whether the tRNA that we have identified represents a minor species of tRNA-leu in *A. pleuropneumoniae*. Regardless, it is possible that tRNA-leu may have any one of a wide range of functions. RpmF is a ribosomal protein whose gene is also part of an operon containing fatty acid biosynthesis enzymes in *E. coli*. Further work will be required to indicate if this is the case in *A. pleuropneumoniae*, although the same clustering of *fab* genes and *rpmF* occurs in *Haemophilus influenzae* [Fleischmann, *et al., Science 269*:496-512 (1995)]. The expression of the *fab* genes is not necessarily dependent on transcripts originating upstream of *rpmF* as there has been a secondary promoter identified within *rpmF* [Zhang and Cronan, Jr., *J Bacteriol. 180*:3295-303 (1998)].

The final class of attenuated mutants includes mutations within genes of unknown function or genes that have not been previously identified. Homologs of *yaeA* and HI0379 have previously been identified in *Escherichia coli* [Blattner, *et al., Science 277*:1453-1474 (1997)] and *Haemophilus influenzae* [Fleischmann, *et al., Science 269*:496-512 (1995)], respectively. The remaining unknowns have been designated Actinobacillus pleuropneumoniae virulence genes (apv). The *apvC* gene shows significant similarity to HI0893, however, the proposed similarity of HI0893 as a transcriptional repressor similar to the fatty acid response regulator Bm3R1 [Palmer, *J Biol Chem. 273*:18109-16 (1998)] is doubtful. The *apvD* gene is also most similar to a putative membrane protein (b0878) with unknown function from *E. coli* [Blattner, *et al., Science 277*:1453-1474 (1997)]. Two other unknowns, *apvA* and *apvB* had no significant matches in the public databases.

Example 11
Safety and Efficacy of *A. pleuropneumoniae* Mutants

Nine groups (n=8) of SPF pigs (4-5 weeks old, 3-10 kg) were used to determine the safety and efficacy of seven *A. pleuropneumoniae* mutants as live attenuated vaccine strains. Seven groups were infected intranasally with 10^{10} CFU of each mutant on day 1. One group was vaccinated on days 1 and 15 with the commercially available vaccine Pleuromune (Bayer), and one naive group was not vaccinated. On day 29, all groups were challenged intranaslally with 1-5 x 10^5 CFU per

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pig of wild type APP225. All surviving animals were euthanized and necropsied on day 42 of the study. Results are shown in Table 4.

Table 4
Efficacy of *A. pleuropneumoniae* Mutants

Vaccine	% Mortality following intranasal challenge	
	Vaccination	Challenge
Pleuromune	0	37.5
exbB	0	0
tig	12.5	0
fkpA	12.5	0
HI0385	50.0	0
pnp	0	0
yaeE	0	0
atpG	0	0
None	N/A	50.0

The *exbB*, *atpG*, *pnp*, and *yaeA* mutants caused no mortality when administered at a dosage of 10^{10} CFU intranasally. The *fkpA* and *tig* mutant groups had one death each and the HI0379 group (highest April 6, 2000CI of the 7 mutants tested shown in Example 9) had four deaths. Wildtype LD_{50} using this model was generally 1 x 10^7 CFU, indicating that each of these mutants is at least 100 fold attenuated and that there is a reasonable correlation between CI and attenuation.

Numerous modifications and variations in the invention as set forth in the above illustrative examples are expected to occur to those skilled in the art. Consequently only such limitations as appear in the appended claims should be placed on the invention.

WHAT IS CLAIMED IS:

1. A gram-negative bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120 122, 124, 126, 128, and 130, or species homologs thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

2. The gram-negative bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

3. The gram-negative bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

4. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.

5. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

6. The gram-negative bacteria of claim 1 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

7. An attenuated *Pasteurellaceae* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124,

54

126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

8. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

9. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

10. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in deletion of all or part of said gene.

11. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

12. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

13. The *Pasteurellaceae* bacteria of claim 7 selected from the group consisting of *Pasteurella haemolytica, Pasteurella multocida, Actinobacillus pleuropneumoniae* and *Haemophilus somnus*.

14. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

15. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

16. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of all or part of said gene.

17. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

18. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

19. The attenuated *Pasteurellaceae* bacteria of claim 13 that is a *P. multocida* bacteria.

20. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

21. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

22. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in deletion of all or part of said gene.

23. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least

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about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

24.   The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

25.   The attenuated *Pasteurellaceae* bacteria of claim 13 that is a *A. pleuropneumoniae* bacteria.

26.   The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

27.   The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

28.   The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in deletion of all or part of said gene.

29.   The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

30.   The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

31. An immunogenic composition comprising the bacteria according to any one of claims 1 through 30.

32. A vaccine composition comprising the immunogenic composition according to claim 31 and a pharmaceutically acceptable carrier.

33. The vaccine composition according to claim 32 further comprising an adjuvant.

34. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

35. A method for producing an attenuated *Pasteurellaceae* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

36. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112,

114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, .

37. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120 122, 124, 126, 128, and 130.

38. A purified and isolated polynucleotide encoding a *Pasteurellaceae*. virulence gene product, or species homolog thereof, selected from the group consisting of:

a) the polynucleotide according to claim 37,

b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a), and

c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

39. A purified and isolated *Pasteurellaceae* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, and 165.

40. The polynucleotide of claim 39 which is a DNA.

41. A vector comprising the DNA of claim 40.

42. The vector of claim 41 that is an expression vector, wherein the DNA is operatively linked to an expression control DNA sequence.

43. A host cell stably transformed or transfected with the DNA of claim 40 in a manner allowing the expression of the encoded polypeptide in said host cell.

44. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 43 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

45. A purified polypeptide produced by the method of claim 44.

46. A purified polypeptide comprising a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, and 165.

47. An antibody that is specifically reactive with the polypeptide of claim 46.

48. The antibody of claim 47 that is a monoclonal antibody.

49. A method of using the monoclonal antibody of claim 39 for identifying a bacteria of claim 1, 7, 13, or 19 comprising the step of contacting an extract of bacteria with said monoclonal antibody and detecting the absence of binding of said monoclonal antibody.

50. A method of identifying an anti-bacterial agent comprising the steps of assaying potential agents for the ability to interfere with expression or activity of gene products represented by the amino acid sequences set forth in any one of SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123,

125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, and 165 and identifying an agent that interferes with expression or activity of said gene products.

51. A method of identifying an anti-bacterial agent comprising the steps of:

a) measuring expression or activity of a gene product as set out in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, and 165

b) contacting the gene product in (a) with a test compound

c) measuring expression or activity of the gene product in the presence of the test compound; and

d) identifying the test compound as an antibacterial agent when expression or activity of the gene product is decreased in the presence of the test compound as compared to expression or activity in the presence of the test compound.

ABSTRACT

Gram negative bacterial virulence genes are identified, thereby allowing the identification of novel anti-bacterial agents that target these virulence genes and their products, and the provision of novel gram negative bacterial mutants useful in vaccines.

<110> Lowery E., David
      Fuller E., Troy
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1

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Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu
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Asn His Pro Leu Leu Ile Pro Val Asn Leu Ala Leu Glu Ser Val Thr
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Leu Leu Ala Lys Pro Val Ser Leu Ala Phe Arg Leu Phe Gly Asn Met
185                 190                 195                 200

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His Gly Pro Arg His Ala Val Gly Pro Leu Ala Leu Thr Ile Phe Cys
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Trp Val Phe Ile Met Asn Ala Ile Asp Leu Ile Pro Val Asp Phe Leu
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Lys Glu Tyr Thr Leu His Pro Phe Asn His Pro Leu Leu Ile Pro Val
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Asn Leu Ala Leu Glu Ser Val Thr Leu Leu Ala Lys Pro Val Ser Leu
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            195                 200                 205

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Gly Ile Phe Met His Leu Ala Trp Ala Ile Phe His Ile Leu Val Ile
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tcgtattggt tcatttgaat cagcactttt agagtatgct aaccataact atgctgattt 240

tatgcgtgag ttaacccaat ctggcaatta caatgatgaa attaaagagt cattaaaagg 300

cattttggat agcttcaaag caaacagtgc gtggtaagtt aacactttaa atggagagac 360

aaa atg gca ggt gct aaa gag ata aga acc aaa atc gcg agt gta aaa   408
    Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys
    1   5   10   15

agt aca caa aaa att act aaa gcg atg gaa atg gtt gct gcc tcg aaa   456
Ser Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys
            20   25   30

atg cgt aaa acg caa gaa cgc atg tct tct tca cgc cct tat tca gaa   504
Met Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu
            35   40   45

aca ata cgt aac gtg att agc cac gtt tcc aaa gca acg att ggt tac   552
Thr Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr
        50   55   60

aag cat cca ttt tta gtg gat cgc gaa gta aaa aaa gtg ggc atg att   600
Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile
        65   70   75

gtt gtg tcc aca gat cgt ggt ctt tgt ggt ggc tta aac gtg aac ttg   648
Val Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu
80   85   90   95

ttt aaa act gta tta aat gaa atg aaa gaa tgg aaa gaa aaa gat gtt   696
Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val
            100   105   110

tcc gtt caa ttg agt tta atc ggt tct aaa tct atc aac ttt ttc caa   744
Ser Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln
            115   120   125

tct ttg gga att aaa att tta acc caa gat tca ggt att ggt gat act   792
Ser Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr
            130   135   140

ccc tct gtt gag cag tta att ggt tca gtc aat tct atg att gat gct   840
Pro Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala
        145   150   155

tat aaa aaa ggg gaa gta gat gtt gtg tat tta gtt tat aac aaa ttt   888
Tyr Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe
160   165   170   175

att aac acg atg tcg caa aag cca gta ttg gaa aaa tta att cca tta   936
Ile Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu
                180   185   190

cca gaa tta gat aat gat gaa tta ggc gaa aga aaa caa gtt tgg gat   984
Pro Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp

4

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tat att tac gaa cct gat gcg aaa gta tta tta gat aat tta ttg gtt   1032
Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val
            210             215                 220

cgt tat tta gaa tct cag gtt tat caa gca gca gtt gaa aac ctt gct   1080
Arg Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala
        225                 230             235

tct gag caa gcc gct cga atg gtc gcc atg aaa gca gca aca gat aac   1128
Ser Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn
240             245                 250                 255

gca ggt aac tta att aat gag tta cag tta gtc tat aac aaa gct cgt   1176
Ala Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg
                260                 265                 270

caa gca agt att aca aat gaa tta aat gaa att gtt gcc ggt gca gca   1224
Gln Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala
                275                 280                 285

gca att taacaaatag aggatcggta atggcaactg gaaaaattgt acaaatcatc   1280
Ala Ile

ggtgcggtta ttgacgttga attcccacaa gatgcagtac caaaagtata tgatgcctta 1340

aatgttgaaa caggtttagt acttgaagtt caacaacaat taggtggtgg tgtagttcgc 1400

tgtatcgcaa tgggatcatc tgatggatta aaacgcggtt taagcgtaac aaatacgaat 1460

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<210> 4
<211> 289
<212> PRT
<213> Pasteurella multocida

<400> 4
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Ser
 1               5                  10                  15

Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met
            20                  25                  30
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5

```
Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu Thr
        35              40                  45

Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr Lys
        50              55                  60

His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile Val
65              70                  75                      80

Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu Phe
                85                  90                  95

Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val Ser
            100             105                 110

Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln Ser
            115             120                 125

Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr Pro
    130                 135                 140

Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala Tyr
145                 150                 155                 160

Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe Ile
                165                 170                 175

Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu Pro
            180             185                 190

Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp Tyr
        195                 200                 205

Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val Arg
        210             215                 220

Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala Ser
225                 230                 235                 240

Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala
                245             250                 255

Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln
            260             265                 270

Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala
        275             280                 285

Ile


<210> 5
<211> 1357
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(813)

<220>
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6

<223> cap5E

<400> 5

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Val Asp Tyr Ile Tyr His Ala Ala Ala Leu Lys Gln Val Pro Ser Cys
 1               5                  10                  15

gag ttt tat ccg tta gag gca gtg aaa acc aat att tta ggt acg gca      96
Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala
              20                  25                  30

aat gtc tta gaa gcc gcc atc caa aac cag ata aaa cgc gtc gtc tgt     144
Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys
          35                  40                  45

ctt agc aca gat aaa gcg gtg tac cca att aat gcg atg ggc att tct     192
Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser
      50                  55                  60

aaa gca atg atg gaa aaa gtc atc atc gca aaa tcg cgt aac cta gaa     240
Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
 65                  70                  75                  80

ggc aca cca acg aca atc tgt tgt act cgc tat ggc aat gtc atg gca     288
Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala
                  85                  90                  95

tcg cgt ggt tcg gtt atc cca tta ttt gtc gat caa ata cgt caa ggc     336
Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
             100                 105                 110

aag cct ttt act att act gat cct gag atg aca cgc ttt atg atg aca     384
Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr
             115                 120                 125

ttg gaa gat gct gtg gat tta gtc cta tat gca ttt aaa aat ggt caa     432
Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln
         130                 135                 140

aat ggt gat gtt ttt gta caa aaa gcc ccc gca gca acc att ggt acc     480
Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr
145                 150                 155                 160

ctt gcc aaa gca att acc gaa tta tta tct gtc cca aat cac cct att     528
Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile
                 165                 170                 175

tcc att ata ggt acg cgt cat gga gag aaa gca ttc gaa gct tta tta     576
Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu
             180                 185                 190

agc cgt gaa gaa atg gtt cat gca att aat gaa ggt aat tat tat cgc     624
Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
             195                 200                 205

atc cca gcc gat caa cgc agt tta aat tac agt aaa tat gtc gaa aaa     672
Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
         210                 215                 220

ggg gaa cca aaa att acc gaa gtc acc gac tac aac tca cat aat act     720
Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr
225                 230                 235                 240
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7

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gag cgt ttg act gtc aag gaa atg aag cag tta ctg ctt aaa ctt gaa    768
Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu
            245                 250                 255

ttc ata cag aaa atg att gag ggt gaa tac atc tca ccg gag gta        813
Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val
            260                 265                 270

taaaaatgaa agtcttagta actggttcaa atggttttat tgcgaaaaat ctgattcagt 873

ctttatctga ggaacaagat attgagattt tatgttatca ccgtcaatcc tctgagaaaa 933

cgcttattca tcatgtattg agtgctgatt ggattattca tcttgcgggt gcgaatcgtc 993

cacctgaaga acaagaattt atgacatcaa atacacaatt gacggaaaaa atttgccgta 1053

ttttacagcg tcatcagaaa aaaacgcctt tgttatattc ctctagcatt caagtagaaa 1113

gtcccaaaat aagtacttat tcgcaaacca aattagaaag tgaatatcat gttcatcaat 1173

tacataaaga aaatggtaat ccgatttata tctgccgttt agctaatgtc tttggcaaat 1233

ggtcacgacc tcactataac tcggtagtcg ccacattttg ccataactta attcatgatt 1293

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ttga                                                              1357


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<211> 271
<212> PRT
<213> Pasteurella multocida

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Val Asp Tyr Ile Tyr His Ala Ala Ala Leu Lys Gln Val Pro Ser Cys
  1             5                  10                  15

Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala
            20                  25                  30

Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys
            35                  40                  45

Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser
      50                  55                  60

Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
 65                  70                  75                  80

Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala
                  85                  90                  95

Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
            100                 105                 110

Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr
            115                 120                 125

Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln
      130                 135                 140
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8

```
Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr
145                 150                 155                 160

Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile
            165                 170                 175

Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu
            180                 185                 190

Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
            195                 200                 205

Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
        210                 215                 220

Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr
225                 230                 235                 240

Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu
            245                 250                 255

Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val
            260                 265                 270


<210> 7
<211> 6132
<212> DNA
<213> Pasteurella multocida

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<222> (4032)..(4727)

<220>
<223> devB

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cgtactttag caaaagacat gattgatggc ggtaaagtgc attataatgg gcagcgcacg 180

aaacccaata aaacggttga aattggtggt gtgatcaaac ttcgtcaagg taatgacgaa 240

aaagaagtgg aagtgcttgc gctttctacg caacgtcgtg gggcgccaga agcacaattg 300

ttgtatcaag aaacagaaaa aagccttgaa caacgtgcga aaatggcgat tgcacgtaag 360

attaatgcat taacgatgcc gcatcctgat cgtcgcccga taaaaaaga gcggcgtgat 420

ttattgaaat ttaaacatca agatagcttt tcatcttgat gatgtgattt acctactttt 480

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tttatgacag acaacacaga caatgacaaa ctgtatcgct accttttcca agatcgcgcg 600

gtgcgcggtg aatgggtacg gttaaaccaa acgtttactg atacgttaaa tacacatcaa 660

tatccgaaag tcatccaaaa cttgctcggt gaaatgatgg tggcgaccag tttattgacg 720
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9

gcgacgttaa aatttgaagg ggatattact gttcaagtac aaggtgatgg accattaaaa 780

ttagcattag ttaatggcaa tcatcagcag caaattcgcg cattagcgcg tttacaagcg 840

gatgtcagtg atgatatgag tttggcgcaa ttagtcggga aaggggtatt agtgattacg 900

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10

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aaggaaagat c atg aat aca atc att ttt gac agt gca cag cat gcc gta 4070
            Met Asn Thr Ile Ile Phe Asp Ser Ala Gln His Ala Val
             1           5                   10

gag aaa att gca caa gaa ttg tta gcg tat agc tta gaa ggt cgc cct   4118
Glu Lys Ile Ala Gln Glu Leu Leu Ala Tyr Ser Leu Glu Gly Arg Pro
 15                20                  25

gtg cat att tcc tta tcc gga ggc tca acg ccg aaa ttg tta ttt aaa   4166
Val His Ile Ser Leu Ser Gly Gly Ser Thr Pro Lys Leu Leu Phe Lys
 30                35                  40                  45

act tta gct caa gca ccg tat aac acc gag att caa tgg aaa aat ttg   4214
Thr Leu Ala Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu
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11

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cat ttt tgg tgg ggc gat gat cgt atg gtg cca cca acc gat cca gaa   4262
His Phe Trp Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu
            65                  70                  75

agt aat tac ggc gag gtg caa aaa ttg tta ttc gat cat att cag atc   4310
Ser Asn Tyr Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile
        80                  85                  90


cct gca gaa aat att cac cgc att cgt ggt gaa gcc ccc gtt gag agt   4358
Pro Ala Glu Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser
        95                  100                 105

gaa ctt cac cgt ttt gaa caa gcg cta agt gcg gtc att cct ggg caa   4406
Glu Leu His Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln
110                 115                 120                 125

gtt ttt gat tgg att att ttg ggc atg gga acg gac ggg cac acg gcc   4454
Val Phe Asp Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala
                130                 135                 140

tca tta ttc ccg cat caa acc gat ttt gac gat cct cat ttc gcc gtg   4502
Ser Leu Phe Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val
            145                 150                 155

atc gcg aaa cac cct gaa aca ggg caa att cgt att tca aaa aca gcg   4550
Ile Ala Lys His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala
            160                 165                 170

aaa ttg att gaa caa gca aag cgg gtg acc tat ttg gtg aca ggt agc   4598
Lys Leu Ile Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser
        175                 180                 185

agt aaa gcc gag atc tta aaa gaa att caa act act ccg gca gaa caa   4646
Ser Lys Ala Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln
190                 195                 200                 205

ctg cct tat cct gct gcg aaa atc aaa gcg aag cat ggg gtg acg gaa   4694
Leu Pro Tyr Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu
                210                 215                 220

tgg tat ttg gat aag gat gcg gca aaa tta ctg taatgcgtcg tgagattttt 4747
Trp Tyr Leu Asp Lys Asp Ala Ala Lys Leu Leu
                225                 230
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12

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tgatttcgcc cctttagctc gcaaaccgtt acaagaaatg cccgctgtgt taagccaaga 5287

gctaacaagg cttaatcaat tattagaaga agggttaaca aatcacactg ggcgatttaa 5347

tgcaaacctc cagtgctttt ggtcgagtac aatcctcgtt gtcttttttc cgtaattcct 5407

atgatgactt tgccgcttat cgtgcggtgt aaatcgtttt aactggcttt catagcgcga 5467

ttaaagcggc taatcgccca agcaaattag tgctcacaga aagtcgtcat gatattggtt 5527

ttcatgatct caacgtagag accccgcaag gaaaaacctt aattgacaag ctcaacctac 5587

aatttcctct cggtacatgg ttattaattc aaggacattc tggtgtaggg aaaacaacct 5647

tgttaagaac cattgcggga ctatggcctt atgctagtgg gacaattcaa cgtccacaac 5707

aagatactct gtttctttct caaaaacctt atttgccaca aggtcgccta cttgatgccc 5767

tattttatcc tgaactggcg cctgaagacg tgaatgagca acaagttata gacatactcg 5827

cgaaagtaca actcgggcat ttaagcgata aactagaaca agaaaatgat tggacacggg 5887

tactctcttt aggtgaacaa caacgtctgt cgtttgctcg cattttattg cataaaccta 5947

ctgttgtttt cttagatgaa gccactgcca gcatggatga aggactggaa gatgcgatgt 6007

accgcttact gaaagatgaa ctgcctcaga ttactgtgat cagtgttgga caccgttcga 6067

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gtcga                                                                 6132


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<212> PRT
<213> Pasteurella multocida

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Met Asn Thr Ile Ile Phe Asp Ser Ala Gln His Ala Val Glu Lys Ile
 1               5                  10                  15

Ala Gln Glu Leu Leu Ala Tyr Ser Leu Glu Gly Arg Pro Val His Ile
            20                  25                  30

Ser Leu Ser Gly Gly Ser Thr Pro Lys Leu Leu Phe Lys Thr Leu Ala
        35                  40                  45

Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu His Phe Trp
    50                  55                  60

Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu Ser Asn Tyr
65                  70                  75                  80

Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile Pro Ala Glu
                85                  90                  95

Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser Glu Leu His
            100                 105                 110

Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln Val Phe Asp
            115                 120                 125
```

13

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Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala Ser Leu Phe
    130             135             140

Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val Ile Ala Lys
145             150             155             160

His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala Lys Leu Ile
                165             170             175

Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser Ser Lys Ala
            180             185             190

Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln Leu Pro Tyr
        195             200             205

Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu Trp Tyr Leu
    210             215             220

Asp Lys Asp Ala Ala Lys Leu Leu
225             230
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<210> 9
<211> 2438
<212> DNA
<213> Pasteurella multocida

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<222> (1635)..(2396)

<220>
<223> dnaA

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gaagctgcgc accctgatat cgaattatat accgcatcag ttgatagtca cttaaatgaa 180

caaggctata ttattccagg tcttggtgat gccggtgata aaattttttgg cactaaataa 240

tcccaacaca agcggcatct tatgccgctt ttttccgttc aatttatagc gcttacaatc 300

ttaacagctt gaacactata aaatgaaaag ttaattcaga cagagagttg aaacttaaca 360

tgacaaatca aaatcccccct gttcttctag aacaaaatca cgcaaaacaa gccttcgttg 420

ggctacaaat gctttttgtt gccttcggtg ctttagtcct tgttcccctg attacgggtt 480

taaatgccaa tactgcctta ttgaccgcag ggattgggac actcttattc caactttgta 540

ctggacgcca agtcccaatt ttcttagcct cttcctttgc ttttattgca ccaattcaat 600

atggcgtggc aacatggggc attgctacta ctatgggggg gctggtgttt actggactgg 660

tttattttgc cctcagtacg ttagtcaaaa ttaaaggtgc tggtgcttta caaaaagtct 720

ttccgccagt agttgttggt cccgttatta tcatcatcgg tatgggactt gcccctgttg 780

ccgtggacat ggcattaggt aaaaacagca cttatcaata taacgatgcc gtattcgttt 840
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14

cgatggcaac attattgaca acgttaggtg ttgcggtgtt tgctaaaggc atgatgaaat 900

taattcctat catgtttggt attgtcgtcg gctatatcct ctgcttattc ttaggcttaa 960

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tgaactttgg agaagtctcc ttaaaaggga ttagtttatg cgccgttgtc gcgattttac 1560

tcaacttaat cttacccaaa gccaaaaaca ccccaataga agaaatcga taagagaaaa 1620

ttaagggtta agtc ttg ctt aac cct tca ttt ttc gtt tat cct tat tct   1670
              Leu Leu Asn Pro Ser Phe Phe Val Tyr Pro Tyr Ser
               1   5   10

cct ttt ttc gat ttt gta ggt tgc ttt ttg tta gaa aat ttc caa tta   1718
Pro Phe Phe Asp Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu
         15   20   25

cct ttg cct att cat caa ctc gat gat gaa acg ctg gat aat ttc tat   1766
Pro Leu Pro Ile His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr
     30   35   40

ccc gac aat aat tta ttg ttg ctc aat tcg cta cgc aaa aat ttt act   1814
Pro Asp Asn Asn Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr
 45   50   55   60

tgt cta aca caa caa ttt ttt tat att tgg ggc gag caa agc agt ggt   1862
Cys Leu Thr Gln Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly
                 65   70   75

aaa agt cac ctc tta aaa ggc att act cat cat ttt ttc ctt tta cag   1910
Lys Ser His Leu Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln
             80   85   90

cgc ccc gct atc tat gtg ccc tta gaa aaa tcc caa tat ttc tca ccg   1958
Arg Pro Ala Ile Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro
             95   100   105

gcg gta ctc gaa aac tta gaa caa caa caa ttg gtt tgt tta gat aat   2006
Ala Val Leu Glu Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn
         110   115   120

tta cag gca att ata ggc aat act gaa tgg gaa tta gcg att ttt gat   2054
Leu Gln Ala Ile Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp
125   130   135   140

15

```
tta ttt aat cgc ata aaa tct gtt gaa aat aca ctg ctt gtg atc agt   2102
Leu Phe Asn Arg Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser
            145                 150                 155

gca aat caa tcc cca act gca tta cct gta agt tta cct gac tta gct   2150
Ala Asn Gln Ser Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala
            160                 165                 170

tca cgt tta cgc tgg gga gaa agc tat cag ctg gtc ccc tta aat gat   2198
Ser Arg Leu Arg Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp
            175                 180                 185


caa caa aaa atc cat gta ttg caa aaa aat gca cat caa cgt ggt atc   2246
Gln Gln Lys Ile His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile
            190                 195                 200

gaa ctc ccc gat gaa gta gct aat ttt ctt ttg aaa cgc tta gag cgc   2294
Glu Leu Pro Asp Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg
205                 210                 215                 220

gat atg aaa acg tta ttt gaa gca cta agt aaa tta gat aaa gca tca   2342
Asp Met Lys Thr Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser
            225                 230                 235

tta caa gcc caa cgt aaa tta acg att ccc ttt gta aaa gaa att tta   2390
Leu Gln Ala Gln Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu
            240                 245                 250

aag cta taaaaaaga ccacctcttt atcaggtgat ctttcttgtc ga            2438
Lys Leu


<210> 10
<211> 254
<212> PRT
<213> Pasteurella multocida

<400> 10
Leu Leu Asn Pro Ser Phe Phe Val Tyr Pro Tyr Ser Pro Phe Phe Asp
 1               5                  10                  15

Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu Pro Leu Pro Ile
            20                  25                  30

His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr Pro Asp Asn Asn
            35                  40                  45

Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr Cys Leu Thr Gln
        50                  55                  60

Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly Lys Ser His Leu
65                  70                  75                  80

Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln Arg Pro Ala Ile
                85                  90                  95

Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro Ala Val Leu Glu
            100                 105                 110

Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn Leu Gln Ala Ile
            115                 120                 125
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16

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Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp Leu Phe Asn Arg
    130             135             140

Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser Ala Asn Gln Ser
145             150             155             160

Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala Ser Arg Leu Arg
            165             170             175

Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp Gln Gln Lys Ile
            180             185             190


His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile Glu Leu Pro Asp
        195             200             205

Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg Asp Met Lys Thr
    210             215             220

Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser Leu Gln Ala Gln
225             230             235             240

Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu Lys Leu
            245             250


<210> 11
<211> 2060
<212> DNA
<213> Pasteurella multocida

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<221> CDS
<222> (856)..(1389)

<220>
<223> dsbB

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tggggcatct tggcaaagtt tgatcgcaat aatcaacaaa aaatgtcacg acaagatcgt 180

ttgaaacttt ttgtgcaagc tttaattggt atttggttgg ttgttggact cgcattccat 240

ctcgccgccg tcggtatcat tggtttaacg gtgattattt tggctacttc attttgtggt 300

gtcaccagcg agcatgctat tggtaaagcc tttcaggaat ccttaccctt cacagcattg 360

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attcagtttg tgctggctgc cagtgaacat actcagcttg ctcttttcta tatttttaac 480

ggtttgttat ccgccatttc agataatgtg tttgtggcca cagtttatat caatgaaacc 540

aaagcggcat tagaggctgg cttaattgct caaccacaat atgaattact ggcagtagca 600

attaataccg gtaccaatct tccttctgtt gcaaccccaa atggtcaagc cgcattctta 660

tttttattga cctcatcact ggcaccatta attcgtcttt cttatggtag aatggtttat 720
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17

atggcattgc cttataccat cgtattatcc tgtattggtt tattgactgt ggaatatatt 780

ttgcctggcg caaccaatgt gctcattcaa attggtttat taaaaccaat gtaatgacaa 840

gtaaaaggag gaaac atg cta agc ttt ttt aag aca ctc tca aca aaa cga 891
               Met Leu Ser Phe Phe Lys Thr Leu Ser Thr Lys Arg
                1   5   10

agt gca tgg ttt cta ttg ttt agc tca gct tta cta tta gag gct atc 939
Ser Ala Trp Phe Leu Leu Phe Ser Ser Ala Leu Leu Leu Glu Ala Ile
       15   20   25

gct ctt tat ttt caa cat ggc atg ggg ctc gcc cct tgt gtc atg tgt 987
Ala Leu Tyr Phe Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys
       30   35   40

att tac gag agg gta gct att ctt ggc att gct ttc tcc ggt tta ttg 1035
Ile Tyr Glu Arg Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu
45   50   55   60

ggg tta ctc tac ccg agt tcg atg ctt ttg cgc ctt gtg gcg tta tta 1083
Gly Leu Leu Tyr Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu
              65   70   75

att ggt tta agc agt gca atc aaa ggc tta atg att agc atc acc cat 1131
Ile Gly Leu Ser Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His
           80   85   90

tta gat cta caa ctt tac cct gca cct tgg aaa caa tgt tca gcg gtg 1179
Leu Asp Leu Gln Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val
          95   100   105

gca gaa ttt ccc gag act tta ccc tta gat cag tgg ttt cct gca ctc 1227
Ala Glu Phe Pro Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu
      110   115   120

ttc ctc cct tca ggc tca tgc agt gaa gta aca tgg caa ttt ctc ggc 1275
Phe Leu Pro Ser Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly
125   130   135   140

ttt tct atg gtg caa tgg atc gtc gtc att ttt gca ctc tat acc tta 1323
Phe Ser Met Val Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu
             145   150   155

tta ctt gct ctc att ttc atc agc caa gtc aaa cgt cta aaa ccc aag 1371
Leu Leu Ala Leu Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys
           160   165   170

cag cgc aga ctc ttt cat taagtcataa aaaatggtgc gataaagcac 1419
Gln Arg Arg Leu Phe His
      175

cattttcat ttctcgttcg gtatagatta aatttcttgc acgacaaact gcagggaatg 1479

tcttgctaat aatcttgctt tacgctgctt taagcgtttt aaacgtaatg cgcgtccttg 1539

tgataaacga tataattttt ttgtcggctt caaaaagctt ttacgtctcg ccatactctt 1599

cctcttattg tgtcgttacg gttgtcgcta acgtatccgt ttctttcttg atttcgttga 1659

tgttttctat ttcggcggct tgtgtatcta atgtttcttc aatttgtgct tgctgtaccc 1719

18

gataataatg cacaatgctg ttcatataac gacggatatt ttccacatag tgatatgctt 1779

catagcctcg cgcatacccg tattttaacc ccgtgtaata gcgttttct gctaatagtg 1839

gcaaattctt cttcacatct aaccaattat cgggatcacc acctaggctc ttggttaaac 1899

ggcgcgcatc taacaaatgc cctaatccca tattatacgc cgctaaggca aaccaaatac 1959

gctcatcttc tttaatcgta tcaggcattt gcgtaataag ccaatgtaaa tattctgaac 2019

cggctttaat actttgttcc ggatccgttc tgtcttgaat t   2060

<210> 12
<211> 178
<212> PRT
<213> Pasteurella multocida

<400> 12
Met Leu Ser Phe Phe Lys Thr Leu Ser Thr Lys Arg Ser Ala Trp Phe
  1   5   10   15

Leu Leu Phe Ser Ser Ala Leu Leu Leu Glu Ala Ile Ala Leu Tyr Phe
                 20   25   30

Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys Ile Tyr Glu Arg
             35   40   45

Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu Gly Leu Leu Tyr
         50   55   60

Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu Ile Gly Leu Ser
 65   70   75   80

Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His Leu Asp Leu Gln
                 85   90   95

Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val Ala Glu Phe Pro
             100   105   110

Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu Phe Leu Pro Ser
             115   120   125

Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly Phe Ser Met Val
     130   135   140

Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu Leu Leu Ala Leu
145   150   155   160

Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys Gln Arg Arg Leu
                 165   170   175

Phe His

<210> 13
<211> 4426
<212> DNA
<213> Pasteurella multocida

<220>

19

<221> CDS
<222> (2756)..(3211)

<220>
<223> exbB

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tttattaata aagtcacgta ccactggtaa cgccacatcc gcttctaata atgccatgcg 120

gacttcacgt agcgtttcct taatattgtc atcagttaaa cgtccacgtc cactaatgtt 180

acgtagcgtt tttgacaagc gatccgacaa attctcaaac atgcaatctt cctatttaat 240

ctcgaaaaaa ttgccctaat tatactgaaa tcccatagat tttcatcctt tgtaataaat 300

ttatagcgat ttcacagtga gaaagttaga atggacggag aacaaaggtg agggaatttc 360

aatgtggctt tcaattttt ccgtgttttt ttatctattg agtgtcttac tcattacccc 420

tatgttgtta aaaattcaag cgggcgaacc cgcatcggtt cccaatagga tgcctttttt 480

aacggcagca ttactcgcca ttcttctgca ctttatcaat cttattcctc tttttaccga 540

tttaaccagc ggtcaaaatt tctcggttat cgaaatcagt tccttaatca gtgttatgac 600

agcaacgatc gccacattag cgttttatt tcgcatacac actttatggt ttttattacc 660

gattatttat tctttcgcca tcattaatct ggtcctcagt accttaatgc cggcgcattt 720

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ttattcggtc tgttcgattg tcgcgttata ttccattcag ttagtttgga tcgatcgcgc 840

cttaaaaaat aaaaaactgc cttttcacc aatgattcca ccgttaatga ccgtagagcg 900

ccatttttt cgtttaatgc tgataggtga aatattactc acgattgtcc tcatttcagg 960

gagctaccat ttatcgaaaa cctttgcccc acaagacatc cagaaagctg tttttctttt 1020

cttggcttgg atagtctttg ggagtgcact ggttggtcat tggaagctcc attggcgtgg 1080

aaaaaaagtg gtgtattatg cgcttttagg tatcattctc ctgactatcg cctattttgg 1140

tagtcgtgta atgcttgaaa tataaacaag atttatttat gctacgccat agtaaaagtg 1200

cggttcaaaa aacgaaaaaa tgaccgcact tttcgatttt tgattaactc gcaaaaggat 1260

gcattttgga cagtattccc cttagtaccc tctttattac actcatcatc ttattgatca 1320

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gttatccaga aaaagtggca ttcacgtcca gtcatttgtt gtccgttttt ctgcgacttt 1680

20

ttaccccgct ggtctattta atgaatttaa ttattcaggg gattttggca ctattacgtc 1740

taaaatcaga taataaatca acctcattaa gcccagagga attacgttcc atcgtaaatg 1800

aatcaggtaa atttattcct tccgcccacc aagaaatgct gttatctatt ttggatttag 1860

aaggggtcac cgtagatgac attatggtgc cacgtaatga cattgggggt attgatattg 1920

acgatgattg gaaagccatt atgcgtcaac ttaaccatgc agcgcacggg cgtgttgtac 1980

tgtataaagg aaatatggat gaaaatattt tggggatgtt acgtgtacgt gaagcctatc 2040

gcttaatgct cgataaaaat gaatttaaca aagaaacttt aatccgtgcc gccgatgaag 2100

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aagaaaggat tggtttagtt gtagatgaat atggtgatat taaaggctta gtcaccttag 2220

aagatatctt agaagagatt gtcggtgaat ttaccacttc aacagcccca tcaattaacg 2280

atgaagttat cccacaatca gacggttcgc ttatcattga gggatccgcc aatttacgtg 2340

atttgaataa attatttgac tggaatctcg ataccgaaga tgcacgtacc ttcaacggct 2400

taattttaga gcatttagaa gaaattccag aagaaggaac ggtatgtgaa attaatgggc 2460

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aatgtttgat ccaacacaac atttattcaa cattggataa ataatcatcc taaatcgcac 2640

gaatttctta tttaccccgt ttttggcttt tgctagaatc ttgcaattga aattaattct 2700

caataccgta taatgttcaa cattattttg cgatacaaat taaaggatta ttaaa atg 2758
                                                                Met
                                                                 1

cca caa tta ttc caa ttc tta caa caa tat att gat tac att att cta 2806
Pro Gln Leu Phe Gln Phe Leu Gln Gln Tyr Ile Asp Tyr Ile Ile Leu
          5   10   15

ggc tta ctt gcc ttc atg agc ttt att atg gtt tgg ctt gtg att gaa 2854
Gly Leu Leu Ala Phe Met Ser Phe Ile Met Val Trp Leu Val Ile Glu
         20   25   30

cgc ttt ctt ttc tta agt cgc gtc aac gtg gca tct tat gaa agc ata 2902
Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser Ile
         35   40   45

cat gaa tta gac att gac tta caa cgc cac ctc aca gct atc tct aca 2950
His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser Thr
 50   55   60   65

atc ggt tct aat gca cct tat gta ggt ttg ctt ggt acc gtc att ggt 2998
Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile Gly
                  70   75   80

att ctc tta act ttc tat gaa tta ggt cac tcc ggt ggc gat att gat 3046
Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile Asp
         85   90   95

21

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gcg gcg gcc att atg gtg cac tta tca tta gcc tta aaa gcc aca gca    3094
Ala Ala Ala Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr Ala
        100                 105                 110

gta ggt att tta gtc gcc att cct gca atg gtg tgt tac aac ggt tta    3142
Val Gly Ile Leu Val Ala Ile Pro Ala Met Val Cys Tyr Asn Gly Leu
    115                 120                 125

gga cgt aaa gtc gaa gtt aat cgt ttg aaa tgg ttt gcc tta aat gag    3190
Gly Arg Lys Val Glu Val Asn Arg Leu Lys Trp Phe Ala Leu Asn Glu
130                 135                 140                 145

aaa aaa gcc aaa caa caa gca tagggagccg tcatgaaaaa gtttgatgaa    3241
Lys Lys Ala Lys Gln Gln Ala
                150

atcaacatta tcccttttat tgacatcatg ttggtactat tggctatcgt tctgattaca 3301

gcctctttta tttcacaagg taaaatccaa gtgaatgtac caaaagcaag ttcaacagtt 3361

gcgtttcgtt cagatgattt agccaaattg ctgactatta cggaaagcgg tgaaattttt 3421

tatcacgata aaccgattac gatagaggca ttggaacaag aaatcagtaa ttgggaaaaa 3481

gatcaaaaag tcaccttgaa ggtagatgca aaatccagtt tccaagattt cgtttctatc 3541

actgatatta tggctaaaaa tgaaattaaa aatgtcgcta tcgtgacggt taaagaaaag 3601

gcatctcaat gatagataaa agtcgttctt gcatcgggtt tgcaatttca ttgcttttttc 3661

acgcaagttt tgtctctttc ctgtattgga ttgtacaaaa agacgatgac agcgcgaatg 3721

gatttgctgc cgatatcatc tcaactcata tttccatgga aatgctggcg gctaccgttt 3781

tagaagaacc agagccggaa ccagagccgg cgcctccggt agtagaacct gaactgccaa 3841

aagaagtagt cgcagatccg acggtaaaac ctgagccacc aaaagaaccc gaaaaaccaa 3901

aagagcctga aaagccaaaa gagaaaccga agaaaaacc aaaagaaaag ccgaaaaaac 3961

cgaagaaaga acaacgtgat ttaccaaagt cagatcgcca aattgattct aattcatcga 4021

tcaatcaaca agcgaccaca acaggcaaca tcacaaccaa taatccgaat ctggtcggta 4081

aaggtaatag cacagatgaa gtcaatgctt atcgctcggc tttacgcaga gaaattgaaa 4141

aacataaacg ctatccaaac cgtgcacgca tgatgcgcaa acaaggtgtg gtaacaatca 4201

cgttccatct taataatgcc ggcgtaatta gtaatgcgcg aatcagcaaa tcttccggct 4261

cagaagaatt agataacgct gcactggtag ctgtcaataa tgcccgtcca attggtccac 4321

tgcctgttgg tatgccaaat gaagtgagcg ttcctgtcag tttcagaatc acaaattaaa 4381

aaagtgcggt aaaatttacc gcacttttt ctctctatta gaatt              4426
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<211> 152
<212> PRT
<213> Pasteurella multocida

22

<400> 14

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Met Pro Gln Leu Phe Gln Phe Leu Gln Gln Tyr Ile Asp Tyr Ile Ile
 1               5                  10                  15

Leu Gly Leu Leu Ala Phe Met Ser Phe Ile Met Val Trp Leu Val Ile
             20                  25                  30

Glu Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser
         35                  40                  45

Ile His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser
     50                  55                  60

Thr Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile
 65                  70                  75                  80

Gly Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile
                 85                  90                  95

Asp Ala Ala Ala Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
             100                 105                 110

Ala Val Gly Ile Leu Val Ala Ile Pro Ala Met Val Cys Tyr Asn Gly
             115                 120                 125

Leu Gly Arg Lys Val Glu Val Asn Arg Leu Lys Trp Phe Ala Leu Asn
     130                 135                 140

Glu Lys Lys Ala Lys Gln Gln Ala
145                 150
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<210> 15
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cccgtcaagt cagcgtaatg tctgccagtg ttacaccaat taaccaattc tgattagaaa 120

aactcatcga gcatcaaatg aaactgcaat ttattcatat caggattatc aataccatat 180

ttttgaaaaa gccgtttctg taatgaagga gaaaactcac cgaggcagtt ccataggatg 240

gcaagatcct ggtatcggtc tgcgattccg actcgtccaa catcaataca acctattaat 300

ttcccctcgt caaaaataag gttatcaagt gagaaatcac catgagtgac gactgaatcc 360

ggtgagaatg gcaaaagctt atgcatttct ttccagactt gttcaacagg ccagccatta 420

cgctcgtcat caaaatcact cgcatcaacc aaaccgttat tcattcgtga ttgcgcctga 480

gcgagacgaa atacgcgatc gctgttaaaa ggacaattac aaacaggaat cga atg 536
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23

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                                                                    Met
                                                                     1

caa ccg gcg cag gaa cac tgc cag cgc atc aac aat att gtt aac caa    584
Gln Pro Ala Gln Glu His Cys Gln Arg Ile Asn Asn Ile Val Asn Gln
              5                  10                  15

gaa aac ggt tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag    632
Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu
          20                  25                  30

cgt tct gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca    680
Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr
      35                  40                  45

gtt cat act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg    728
Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val
50                  55                  60                  65


agt tat aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt    776
Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val
                  70                  75                  80

gcg gta cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg    824
Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu
              85                  90                  95

caa gaa caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc    872
Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile
              100                 105                 110

cgt tct gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca    920
Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser
      115                 120                 125

gaa tca aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga    968
Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly
130                 135                 140                 145

aca ttt aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt   1016
Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe
              150                 155                 160

aac caa aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg   1064
Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr
              165                 170                 175

atg tac tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt   1112
Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly
              180                 185                 190

aat gca tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg   1160
Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu
      195                 200                 205

ttt ggc tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat   1208
Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn
210                 215                 220                 225

ttt agt gct tat cag ctt cta tct cat att cag cat tca cca atg tac   1256
Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr
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24

caa aaa gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc   1304
Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser
            245   250   255

tat gat gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca   1352
Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr
            260   265   270

gat ttc att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa   1400
Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys
    275   280   285

cta gaa ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt   1448
Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg
290   295   300   305

ggt aag ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta   1496
Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu
            310   315   320

cca tca gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa   1544
Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu
            325   330   335

gag gac ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca   1592
Glu Asp Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro
            340   345   350

aac tta ttt att gat aat agt atc caa tta gaa aag aaa aag ttg tct   1640
Asn Leu Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser
            355   360   365

cct att gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa   1688
Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu
370   375   380   385

gaa agc cat tct aat tca tcg gat gac gtg ctt agc atg aat gat gat   1736
Glu Ser His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp
            390   395   400

gag tct gat aca gac gat agc aag tgg agt atg ggc aat gat gag aaa   1784
Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys
            405   410   415

gag atg ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat   1832
Glu Met Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn
            420   425   430

aaa cca cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa   1880
Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu
            435   440   445

ttc ttt gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga   1928
Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly
450   455   460   465

gaa gag ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc   1976
Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr
            470   475   480

25

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aat cta gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga    2024
Asn Leu Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg
            485                 490                 495

gaa aaa gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg    2072
Glu Lys Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu
            500                 505                 510

cag gag tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa    2120
Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys
            515                 520                 525

gca aga ata gaa aaa gca ctt cta caa aaa tca gaa caa caa gaa aaa    2168
Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys
530                 535                 540                 545

cgt gtt gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa    2216
Arg Val Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys
                550                 555                 560

att gct aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa    2264
Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu
            565                 570                 575

att cgc cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag    2312
Ile Arg Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu
            580                 585                 590

aag aaa caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct    2360
Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala
            595                 600                 605

gaa cag aaa caa aaa gct gag gag aaa gtt gca caa gaa aga tta gac    2408
Glu Gln Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp
610                 615                 620                 625

att gaa caa cag aaa gcg tat gaa gaa atg gcg aag cga gag gca gag    2456
Ile Glu Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu
            630                 635                 640

gca tca aaa aat gtt tta ttg aaa gcg att gat gaa gaa cgt cca aaa    2504
Ala Ser Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys
            645                 650                 655

gtg gaa act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa    2552
Val Glu Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln
            660                 665                 670

gat gac tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat    2600
Asp Asp Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn
            675                 680                 685

aca aaa ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat    2648
Thr Lys Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp
690                 695                 700                 705

cat caa gtg att act cgc tcg att gag aaa aaa gta gat aac cac ctt    2696
His Gln Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu
            710                 715                 720

aac caa aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg    2744
Asn Gln Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met
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26

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gac aat tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg    2792
Asp Asn Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala
        740                 745                 750

gca tta act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg    2840
Ala Leu Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp
        755                 760                 765

tat gtc aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt    2888
Tyr Val Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val
770             775                 780                 785

tat ttc gct tct gaa acg ctc gta gaa gcc caa aaa tta caa ggt tta    2936
Tyr Phe Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu
                790                 795                 800

ggc act ggg act atc aga gtt ggt gaa gct aag att aaa gcc aaa gat    2984
Gly Thr Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp
        805                 810                 815

gtg gtg aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg    3032
Val Val Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala
        820                 825                 830

agt aat aaa atc aaa aat caa ggg agt atc tta agt act caa gaa aca    3080
Ser Asn Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr
        835                 840                 845

cgt tta gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca    3128
Arg Leu Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala
850             855                 860                 865

aat gat gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa    3176
Asn Asp Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu
                870                 875                 880

ggt cat tta cat ctt gaa aca gat aag gat tca act att gat gta caa    3224
Gly His Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln
                885                 890                 895

gca tcg gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg    3272
Ala Ser Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val
        900                 905                 910

aat ctc aaa aat aca tac aat act aaa cat gcc tac cgt gag aaa ttc    3320
Asn Leu Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe
        915                 920                 925

tcg ccg agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa    3368
Ser Pro Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys
930                 935                 940                 945

gtc cca ctt tta ggc gtg tcg tct cca tcc agt tat tca gag cat act    3416
Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His Thr
                950                 955                 960

agt gag gca act tca gag gga tca atc ttc gaa gta ggg cac tta cat    3464
Ser Glu Ala Thr Ser Glu Gly Ser Ile Phe Glu Val Gly His Leu His
                965                 970                 975
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27

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ctt gcg gta gac aga gat gtg aac caa gcg ggg agt aaa att aag gct       3512
Leu Ala Val Asp Arg Asp Val Asn Gln Ala Gly Ser Lys Ile Lys Ala
        980                 985                 990


aag tat acc act ggt gtt gtg aaa ggg aac ttt aat act gaa gcg ggc       3560
Lys Tyr Thr Thr Gly Val Val Lys Gly Asn Phe Asn Thr Glu Ala Gly
        995                 1000                1005


aag aat att aaa cat gtc gaa aaa gaa gaa tat agt tca cag cta ttt       3608
Lys Asn Ile Lys His Val Glu Lys Glu Glu Tyr Ser Ser Gln Leu Phe
1010                1015                1020                1025


gct tca gca cac gcg agt ggt ggt ggc acc tca gtt cgt tat gac tat       3656
Ala Ser Ala His Ala Ser Gly Gly Gly Thr Ser Val Arg Tyr Asp Tyr
                1030                1035                1040


aac agc caa gat ggt ggc aat gcc tct gtt ggt gtt ccg aca aac cat       3704
Asn Ser Gln Asp Gly Gly Asn Ala Ser Val Gly Val Pro Thr Asn His
                1045                1050                1055


act gga gtt ggg gca gag gca gga atg tca ttc acc cat acc aaa gac       3752
Thr Gly Val Gly Ala Glu Ala Gly Met Ser Phe Thr His Thr Lys Asp
        1060                1065                1070


aaa gaa aca ctg ctc act cac acc aat agt gaa tta caa gtc aaa cat       3800
Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys His
        1075                1080                1085


ggg aaa tta cat gtg ctt ggt tat gcc gat att ggt gga gta gat att       3848
Gly Lys Leu His Val Leu Gly Tyr Ala Asp Ile Gly Gly Val Asp Ile
1090                1095                1100                1105


aat act aaa cta cca gaa gat gca caa agc aaa gca cag aaa gag ata       3896
Asn Thr Lys Leu Pro Glu Asp Ala Gln Ser Lys Ala Gln Lys Glu Ile
                1110                1115                1120


gcg gct agc aag cca gag aag acc gag caa tct gca cag gat gtg gct       3944
Ala Ala Ser Lys Pro Glu Lys Thr Glu Gln Ser Ala Gln Asp Val Ala
                1125                1130                1135


caa gct caa tca aat gcc aat aag gat aag gaa aat aaa gcc cca gaa       3992
Gln Ala Gln Ser Asn Ala Asn Lys Asp Lys Glu Asn Lys Ala Pro Glu
        1140                1145                1150


ata aaa gaa tta tca gag gct gaa atc gcg gat ctc atg tca gaa aaa       4040
Ile Lys Glu Leu Ser Glu Ala Glu Ile Ala Asp Leu Met Ser Glu Lys
        1155                1160                1165


tca aaa gcg tat ttt gat gat ttt gca gag caa gcg aaa aaa gca cct       4088
Ser Lys Ala Tyr Phe Asp Asp Phe Ala Glu Gln Ala Lys Lys Ala Pro
1170                1175                1180                1185


gaa aac aat cga ttt gaa ttg tct gcg aaa gaa att aag tcg agc aaa       4136
Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser Lys
                1190                1195                1200


caa aaa gac caa tat gat cat gag tct gaa cgg acg act ttt aaa gtt       4184
Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys Val
                1205                1210                1215


gga cct gaa gcg gag gct cat tct gcg gtt gcc gat atg gtg agc cat       4232
Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser His
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28

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tta gtg aaa gaa tat aga gat gca caa aat ggg act aaa caa gac ggt   4280
Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp Gly
  1235                1240                1245

aca gta gca tta caa cat gct agt gat gtc tta aat att gtg acg ggg   4328
Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr Gly
1250                1255                1260                1265

gat tta gcg ggg agt tca gct aaa ttg tct gtt gaa aga aca cat gag   4376
Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His Glu
                1270                1275                1280

aca aaa cga acg aca gaa acg ggg gat att gtt act aag att ggt ggc   4424
Thr Lys Arg Thr Thr Glu Thr Gly Asp Ile Val Thr Lys Ile Gly Gly
           1285                1290                1295

aat gtc aca ctg tca gca cgc agt ggt agt gtg aac ctt aaa aat gta   4472
Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn Val
          1300                1305                1310

caa agt gat gaa caa gct aat ttg acc tta aga gca aaa gaa gat gtg   4520
Gln Ser Asp Glu Gln Ala Asn Leu Thr Leu Arg Ala Lys Glu Asp Val
     1315                1320                1325

aat gtg ctg tct ggt gaa aaa aca cga gaa acc aca gaa aca gta tca   4568
Asn Val Leu Ser Gly Glu Lys Thr Arg Glu Thr Thr Glu Thr Val Ser
1330                1335                1340                1345

aga cag aaa ctt tct cat ggt gtg aac gca ggt tgc agt atg atg agt   4616
Arg Gln Lys Leu Ser His Gly Val Asn Ala Gly Cys Ser Met Met Ser
                1350                1355                1360

ggc gcc tgt act gcc ggt gtt agc aca tca ctt gaa gga aat gaa agc   4664
Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu Ser
           1365                1370                1375

tat acg tca gaa cgt gaa acg gct caa aat aac agt ttc tta aaa gca   4712
Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys Ala
          1380                1385                1390

cgc aac atg aaa gtt gaa gca ggt cgc gat ttt aat gtt gtc agt tcg   4760
Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser Ser
     1395                1400                1405

aat att gat gca gat aag ctc gat ctc cac gtt aaa gga aaa acg aat   4808
Asn Ile Asp Ala Asp Lys Leu Asp Leu His Val Lys Gly Lys Thr Asn
1410                1415                1420                1425

gtg gta tcc aaa caa gat acg tta caa aaa gtg acg cat gga gtt gac   4856
Val Val Ser Lys Gln Asp Thr Leu Gln Lys Val Thr His Gly Val Asp
                1430                1435                1440

tat aat ctt tcc gct ggc gtt gca ctt tct agt gca aca att gct acc   4904
Tyr Asn Leu Ser Ala Gly Val Ala Leu Ser Ser Ala Thr Ile Ala Thr
          1445                1450                1455

cca acc ggt aat gtt ggt ttc ggt tat acc aat gag acc gaa agc aag   4952
Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser Lys
     1460                1465                1470
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29

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cgg acg gtt aat caa caa gca ggg att aaa gcg aat aaa att aca ggg    5000
Arg Thr Val Asn Gln Gln Ala Gly Ile Lys Ala Asn Lys Ile Thr Gly
    1475             1480             1485

caa acg cat gac tta aat ctt gag ggg gga tat ctt gtc agc aac gat    5048
Gln Thr His Asp Leu Asn Leu Glu Gly Gly Tyr Leu Val Ser Asn Asp
1490             1495             1500             1505

aag gat aat cag ctg aaa gtt acc ggc gat gtc aca act aaa gcc ctt    5096
Lys Asp Asn Gln Leu Lys Val Thr Gly Asp Val Thr Thr Lys Ala Leu
            1510             1515             1520

cac gat caa cat gat aaa gat ggt gga aca ttt ggt tta tct gtg ggt    5144
His Asp Gln His Asp Lys Asp Gly Gly Thr Phe Gly Leu Ser Val Gly
            1525             1530             1535

atc agt gaa cgt ggt act acc gcc ttt aat gta cga ggt ggg cga gct    5192
Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Gly Arg Ala
        1540             1545             1550

gaa cag aaa cac tat aat gca acg cag aaa tcc act ctt tct ggc gtg    5240
Glu Gln Lys His Tyr Asn Ala Thr Gln Lys Ser Thr Leu Ser Gly Val
    1555             1560             1565

gat acc tct caa gcg aat gta tca ggt caa gtg aat aca gat tta acc    5288
Asp Thr Ser Gln Ala Asn Val Ser Gly Gln Val Asn Thr Asp Leu Thr
1570             1575             1580             1585

aag gca aaa gct gtc aca cgt gat gat act tac gca agt acg caa ttt    5336
Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln Phe
            1590             1595             1600

agt ttt gaa gtg gca gat att gtg gaa tta gga cag aga gcg aaa aac    5384
Ser Phe Glu Val Ala Asp Ile Val Glu Leu Gly Gln Arg Ala Lys Asn
            1605             1610             1615

aag ctg tca gca cca aac aat gac acc gat atg gcg tca ggc tcc aca    5432
Lys Leu Ser Ala Pro Asn Asn Asp Thr Asp Met Ala Ser Gly Ser Thr
            1620             1625             1630

tta cgc tcg cgt tct act aca gaa gaa gca gat gta cca aca aca aga    5480
Leu Arg Ser Arg Ser Thr Thr Glu Glu Ala Asp Val Pro Thr Thr Arg
        1635             1640             1645

tcg cgt gta acg gat gag gcg gat tct gta tcc gtg aaa aat ccg att    5528
Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro Ile
1650             1655             1660             1665

tat gaa agt gca gat gct gtt gta cca aca cca cgt agt aga aat gtg    5576
Tyr Glu Ser Ala Asp Ala Val Val Pro Thr Pro Arg Ser Arg Asn Val
            1670             1675             1680

gac agt acc gat ctt gtg gac aat cca ctg tat gct agt gcc act aca    5624
Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr Thr
        1685             1690             1695

aaa gca aac atc cat gat tat gaa gaa att cca gcc gtt tat agc aaa    5672
Lys Ala Asn Ile His Asp Tyr Glu Glu Ile Pro Ala Val Tyr Ser Lys
        1700             1705             1710

gtc ggt gat aac aat gct gat ctt gtt cgt cat aaa acg gca act agt    5720
Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr Ser
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                1715                    1720                    1725

      gat gag cat ctt tat gca gag att aat gaa cca aca tat agc cgt gtt      5768
      Asp Glu His Leu Tyr Ala Glu Ile Asn Glu Pro Thr Tyr Ser Arg Val
      1730                    1735                    1740                1745

      ggt gat aaa aat gca gat atg aga cgt cat aac gcg gca ggt aca aca      5816
      Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr Thr
                      1750                    1755                    1760

      gac tat gcc gat gtc gtg caa gca cat aca aga aag gca gat gat cca      5864
      Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp Pro
              1765                    1770                    1775

      cta cca gca tta ccg aat cag ggt aaa gca aga acg gta aac gac ggt      5912
      Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp Gly
                  1780                    1785                    1790

      tca gag cat att tat act gat att agc gac gtg ggc act caa act aaa      5960
      Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr Lys
                1795                    1800                    1805

      gct att gat agt act tat gca aca gta ggc atg ccg aaa gcg aat gcc      6008
      Ala Ile Asp Ser Thr Tyr Ala Thr Val Gly Met Pro Lys Ala Asn Ala
      1810                    1815                    1820                1825

      gtt aac ttg ata ggg caa aat ggc tta ggc agc att tat cac agc cca      6056
      Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser Pro
                      1830                    1835                    1840

      gac agt gct tat aaa aca tgg caa ttg ctt gat caa ttt gcc aac aaa      6104
      Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn Lys
                      1845                    1850                    1855

      ggc gga gat gcg gtc ttc tta cgc cct gca aca gaa atg aaa tgt gca      6152
      Gly Gly Asp Ala Val Phe Leu Arg Pro Ala Thr Glu Met Lys Cys Ala
                  1860                    1865                    1870

      ggt gca cct tta aaa tat acc ttt atc gtg cgt gat tat ttg ctc aga      6200
      Gly Ala Pro Leu Lys Tyr Thr Phe Ile Val Arg Asp Tyr Leu Leu Arg
                1875                    1880                    1885

      cgc cat acc tta gat aaa tca aga tta ttt tat aac gca cat aat aaa      6248
      Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn Lys
      1890                    1895                    1900                1905

      acc tta ttt agc gtg cct atc gtt gat gca aaa gtc aaa atg ctg ttt      6296
      Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu Phe
                      1910                    1915                    1920

      gct gaa aaa aat atc caa gtc aat tac gat cgt agc ctt aca gcc att      6344
      Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala Ile
                      1925                    1930                    1935

      gat ctg agt aaa cgt att gcg acc ttt aat agc cca gaa gga gtt gta      6392
      Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val Val
                  1940                    1945                    1950

      gaa gtc cct tat gat ttt att aat gtg gta cct cca atg cga gca cct      6440
      Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala Pro
                  1955                    1960                    1965
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gat gcc gtt cgt caa tca gca ctc gcg tgg caa gaa gga aaa tgg gct    6488
Asp Ala Val Arg Gln Ser Ala Leu Ala Trp Gln Glu Gly Lys Trp Ala
1970                1975                1980                1985

aac gat ggt tgg gtt gaa gta gaa aaa cat acc ttg cgt cac cgt cgt    6536
Asn Asp Gly Trp Val Glu Val Glu Lys His Thr Leu Arg His Arg Arg
                1990                1995                2000

tat gcc aat gtg ttt gct gtg ggt gat gtg gca ggg gtc cca aaa ggc    6584
Tyr Ala Asn Val Phe Ala Val Gly Asp Val Ala Gly Val Pro Lys Gly
                2005                2010                2015

aaa acg gct gcc agt gtc aaa tgg caa gtt cct gtt gca gtg gca cat    6632
Lys Thr Ala Ala Ser Val Lys Trp Gln Val Pro Val Ala Val Ala His
            2020                2025                2030

tta ctc gca gaa tta gag ggc aaa cct tgt gat gaa att tac aac ggt    6680
Leu Leu Ala Glu Leu Glu Gly Lys Pro Cys Asp Glu Ile Tyr Asn Gly
    2035                2040                2045

tat aca tct tgt cca tta att act caa tta gga aag ggg atg cta gta    6728
Tyr Thr Ser Cys Pro Leu Ile Thr Gln Leu Gly Lys Gly Met Leu Val
2050                2055                2060                2065

gaa ttt gat tat aac aac cac tta aca cct tct ttc ccc ggt gta ata    6776
Glu Phe Asp Tyr Asn Asn His Leu Thr Pro Ser Phe Pro Gly Val Ile
                2070                2075                2080

gcg cca tta gaa gaa ctg tgg gca aca tgg gca att aaa aca tta ggt    6824
Ala Pro Leu Glu Glu Leu Trp Ala Thr Trp Ala Ile Lys Thr Leu Gly
                2085                2090                2095

tta aaa ccc act tat tta ggt atg tta cgt gga tta gct taaggagcgt    6873
Leu Lys Pro Thr Tyr Leu Gly Met Leu Arg Gly Leu Ala
            2100                2105                2110

tga                                                                 6876


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Gln Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala
                20                  25                  30

Glu Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu
            35                  40                  45

Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn
        50                  55                  60

Val Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg
65                  70                  75                  80

Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn
                85                  90                  95
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Leu Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala
        100                 105                 110

Ile Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser
        115             120                 125

Ser Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys
    130             135                 140

Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala
145                 150                 155                 160

Phe Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile
                165                 170                 175

Thr Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser
            180                 185                 190

Gly Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala
            195                 200                 205

Leu Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu
    210                 215                 220

Asn Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met
225                 230                 235                 240

Tyr Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys
                245                 250                 255

Ser Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro
            260                 265                 270

Thr Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly
            275                 280                 285

Lys Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu
    290                 295                 300

Arg Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser
305                 310                 315                 320

Leu Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu
                325                 330                 335

Glu Glu Asp Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met
            340                 345                 350

Pro Asn Leu Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu
            355                 360                 365

Ser Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile
    370                 375                 380

Glu Glu Ser His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp
385                 390                 395                 400

Asp Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu
            405                 410                 415

Lys Glu Met Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly
            420                 425                 430
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Asn Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp
        435   440   445

Glu Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu
        450   455   460

Gly Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser
465   470   475   480

Thr Asn Leu Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys
                485   490   495

Arg Glu Lys Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys
            500   505   510

Leu Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln
        515   520   525

Lys Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu
        530   535   540

Lys Arg Val Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp
545   550   555   560

Lys Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu
                565   570   575

Glu Ile Arg Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu
            580   585   590

Glu Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln
            595   600   605

Ala Glu Gln Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu
    610   615   620

Asp Ile Glu Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala
625   630   635   640

Glu Ala Ser Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro
            645   650   655

Lys Val Glu Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn
            660   665   670

Gln Asp Asp Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu
        675   680   685

Asn Thr Lys Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe
    690   695   700

Asp His Gln Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His
705   710   715   720

Leu Asn Gln Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu
            725   730   735

Met Asp Asn Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly
            740   745   750

Ala Ala Leu Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val
        755   760   765

34

Trp Tyr Val Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys
    770   775   780

Val Tyr Phe Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly
785   790   795   800

Leu Gly Thr Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys
            805   810   815

Asp Val Val Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu
            820   825   830

Ala Ser Asn Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu
        835   840   845

Thr Arg Leu Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe
    850   855   860

Ala Asn Asp Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr
865   870   875   880

Glu Gly His Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val
            885   890   895

Gln Ala Ser Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp
        900   905   910

Val Asn Leu Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys
        915   920   925

Phe Ser Pro Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu
    930   935   940

Lys Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His
945   950   955   960

Thr Ser Glu Ala Thr Ser Glu Gly Ser Ile Phe Glu Val Gly His Leu
            965   970   975

His Leu Ala Val Asp Arg Asp Val Asn Gln Ala Gly Ser Lys Ile Lys
            980   985   990

Ala Lys Tyr Thr Thr Gly Val Val Lys Gly Asn Phe Asn Thr Glu Ala
        995   1000   1005

Gly Lys Asn Ile Lys His Val Glu Lys Glu Glu Tyr Ser Ser Gln Leu
    1010   1015   1020

Phe Ala Ser Ala His Ala Ser Gly Gly Gly Thr Ser Val Arg Tyr Asp
025   1030   1035   1040

Tyr Asn Ser Gln Asp Gly Gly Asn Ala Ser Val Gly Val Pro Thr Asn
            1045   1050   1055

His Thr Gly Val Gly Ala Glu Ala Gly Met Ser Phe Thr His Thr Lys
            1060   1065   1070

Asp Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys
    1075   1080   1085

His Gly Lys Leu His Val Leu Gly Tyr Ala Asp Ile Gly Gly Val Asp
    1090   1095   1100

35

Ile Asn Thr Lys Leu Pro Glu Asp Ala Gln Ser Lys Ala Gln Lys Glu
105   1110   1115   1120

Ile Ala Ala Ser Lys Pro Glu Lys Thr Glu Gln Ser Ala Gln Asp Val
              1125   1130   1135

Ala Gln Ala Gln Ser Asn Ala Asn Lys Asp Lys Glu Asn Lys Ala Pro
              1140   1145   1150

Glu Ile Lys Glu Leu Ser Glu Ala Glu Ile Ala Asp Leu Met Ser Glu
              1155   1160   1165

Lys Ser Lys Ala Tyr Phe Asp Asp Phe Ala Glu Gln Ala Lys Lys Ala
              1170   1175   1180

Pro Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser
185   1190   1195   1200

Lys Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys
              1205   1210   1215

Val Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser
              1220   1225   1230

His Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp
              1235   1240   1245

Gly Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr
              1250   1255   1260

Gly Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His
265   1270   1275   1280

Glu Thr Lys Arg Thr Thr Glu Thr Gly Asp Ile Val Thr Lys Ile Gly
              1285   1290   1295

Gly Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn
              1300   1305   1310

Val Gln Ser Asp Glu Gln Ala Asn Leu Thr Leu Arg Ala Lys Glu Asp
              1315   1320   1325

Val Asn Val Leu Ser Gly Glu Lys Thr Arg Glu Thr Thr Glu Thr Val
              1330   1335   1340

Ser Arg Gln Lys Leu Ser His Gly Val Asn Ala Gly Cys Ser Met Met
345   1350   1355   1360

Ser Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu
              1365   1370   1375

Ser Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys
              1380   1385   1390

Ala Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser
              1395   1400   1405

Ser Asn Ile Asp Ala Asp Lys Leu Asp Leu His Val Lys Gly Lys Thr
              1410   1415   1420

Asn Val Val Ser Lys Gln Asp Thr Leu Gln Lys Val Thr His Gly Val
425   1430   1435   1440

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Asp Tyr Asn Leu Ser Ala Gly Val Ala Leu Ser Ser Ala Thr Ile Ala
        1445                1450                1455

Thr Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser
        1460                1465                1470

Lys Arg Thr Val Asn Gln Gln Ala Gly Ile Lys Ala Asn Lys Ile Thr
        1475                1480                1485

Gly Gln Thr His Asp Leu Asn Leu Glu Gly Gly Tyr Leu Val Ser Asn
        1490                1495                1500

Asp Lys Asp Asn Gln Leu Lys Val Thr Gly Asp Val Thr Thr Lys Ala
505                 1510                1515                1520

Leu His Asp Gln His Asp Lys Asp Gly Gly Thr Phe Gly Leu Ser Val
                1525                1530                1535

Gly Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Gly Arg
                1540                1545                1550

Ala Glu Gln Lys His Tyr Asn Ala Thr Gln Lys Ser Thr Leu Ser Gly
                1555                1560                1565

Val Asp Thr Ser Gln Ala Asn Val Ser Gly Gln Val Asn Thr Asp Leu
        1570                1575                1580

Thr Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln
585                 1590                1595                1600

Phe Ser Phe Glu Val Ala Asp Ile Val Glu Leu Gly Gln Arg Ala Lys
                1605                1610                1615

Asn Lys Leu Ser Ala Pro Asn Asn Asp Thr Asp Met Ala Ser Gly Ser
                1620                1625                1630

Thr Leu Arg Ser Arg Ser Thr Thr Glu Glu Ala Asp Val Pro Thr Thr
        1635                1640                1645

Arg Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro
        1650                1655                1660

Ile Tyr Glu Ser Ala Asp Ala Val Val Pro Thr Pro Arg Ser Arg Asn
665                 1670                1675                1680

Val Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr
                1685                1690                1695

Thr Lys Ala Asn Ile His Asp Tyr Glu Glu Ile Pro Ala Val Tyr Ser
        1700                1705                1710

Lys Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr
        1715                1720                1725

Ser Asp Glu His Leu Tyr Ala Glu Ile Asn Glu Pro Thr Tyr Ser Arg
        1730                1735                1740

Val Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr
745                 1750                1755                1760

Thr Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp
                1765                1770                1775
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Pro Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp
        1780                1785                1790

Gly Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr
        1795                1800                1805

Lys Ala Ile Asp Ser Thr Tyr Ala Thr Val Gly Met Pro Lys Ala Asn
        1810                1815                1820

Ala Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser
825                1830                1835                1840

Pro Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn
        1845                1850                1855

Lys Gly Gly Asp Ala Val Phe Leu Arg Pro Ala Thr Glu Met Lys Cys
        1860                1865                1870

Ala Gly Ala Pro Leu Lys Tyr Thr Phe Ile Val Arg Asp Tyr Leu Leu
        1875                1880                1885

Arg Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn
        1890                1895                1900

Lys Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu
905                1910                1915                1920

Phe Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala
        1925                1930                1935

Ile Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val
        1940                1945                1950

Val Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala
        1955                1960                1965

Pro Asp Ala Val Arg Gln Ser Ala Leu Ala Trp Gln Glu Gly Lys Trp
        1970                1975                1980

Ala Asn Asp Gly Trp Val Glu Val Glu Lys His Thr Leu Arg His Arg
985                1990                1995                2000

Arg Tyr Ala Asn Val Phe Ala Val Gly Asp Val Ala Gly Val Pro Lys
            2005                2010                2015

Gly Lys Thr Ala Ala Ser Val Lys Trp Gln Val Pro Val Ala Val Ala
        2020                2025                2030

His Leu Leu Ala Glu Leu Glu Gly Lys Pro Cys Asp Glu Ile Tyr Asn
        2035                2040                2045

Gly Tyr Thr Ser Cys Pro Leu Ile Thr Gln Leu Gly Lys Gly Met Leu
        2050                2055                2060

Val Glu Phe Asp Tyr Asn Asn His Leu Thr Pro Ser Phe Pro Gly Val
065                2070                2075                2080

Ile Ala Pro Leu Glu Glu Leu Trp Ala Thr Trp Ala Ile Lys Thr Leu
            2085                2090                2095

Gly Leu Lys Pro Thr Tyr Leu Gly Met Leu Arg Gly Leu Ala
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38

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taccgttctg gctacgtgac aagtgcaatt ggtttaaaaa attcaaaaat cagcaatggc 180

gatcttgaat ttattgtact gtggggaaga actcgcgatc tgtttgtgaa tggggagaaa 240

ccaacccgtt ttagagataa aacaatgtta tcagtcctac ccaatttaat cggaaatcgc 300

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acagtgaatg tggttgcaag tgaagaaaaa ggcagctcaa atctaaatat tgaaagacaa 420

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39

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                                         Met Asn Lys Asn Arg Tyr
                                          1                   5

aaa ctc att ttt agt caa gtc aaa ggt tgt ctc gtt cct gtg gca gaa   1544
Lys Leu Ile Phe Ser Gln Val Lys Gly Cys Leu Val Pro Val Ala Glu
            10                  15                  20

tgt att aac tca gct att agc aat ggt tca tct gat tca aca tcc aca   1592
Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser Ser Asp Ser Thr Ser Thr
            25                  30                  35

tca gaa caa gtt gaa gag gaa cct ttc ctt cta gaa caa tat tca ctt   1640
Ser Glu Gln Val Glu Glu Glu Pro Phe Leu Leu Glu Gln Tyr Ser Leu
        40                  45                  50

tcc tcc gtg tct tta tta gta aaa agc acg ttc aat cct gtt tcg tat   1688
Ser Ser Val Ser Leu Leu Val Lys Ser Thr Phe Asn Pro Val Ser Tyr
55                  60                  65                  70

gca atg caa ttg act tgg aaa cag ctt tct att tta ttt tta act gtg   1736
Ala Met Gln Leu Thr Trp Lys Gln Leu Ser Ile Leu Phe Leu Thr Val
                75                  80                  85

att tct gtt cct gtt ttg gct gag gga aaa ggg gat gaa aga aat caa   1784
Ile Ser Val Pro Val Leu Ala Glu Gly Lys Gly Asp Glu Arg Asn Gln
            90                  95                  100

tta aca gtg att gat aat agc gat cat att aaa tta gat gca tct aat   1832
Leu Thr Val Ile Asp Asn Ser Asp His Ile Lys Leu Asp Ala Ser Asn
            105                 110                 115

ctt gct ggt aat gat aaa aca aaa atc tat caa gca gaa aat aaa gtt   1880
Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr Gln Ala Glu Asn Lys Val
        120                 125                 130

ctg gtt att gat att gct aaa cca aat ggg aaa ggg att tca gat aac   1928
Leu Val Ile Asp Ile Ala Lys Pro Asn Gly Lys Gly Ile Ser Asp Asn
135                 140                 145                 150

cgt ttt gaa aaa ttt aat att cca aat agc gcg gtg ttt aat aat aat   1976
Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser Ala Val Phe Asn Asn Asn
                155                 160                 165

ggg act gaa gcg cag gca aga tca aca tta att ggt tac att ccg caa   2024
Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu Ile Gly Tyr Ile Pro Gln
                170                 175                 180

aat caa aat tta agg gga ggg aaa gaa gct gat gtt ata tta aat caa   2072
Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala Asp Val Ile Leu Asn Gln
            185                 190                 195

gtg aca ggt cct caa gaa agt aaa att gtt ggc gcg ctt gaa gta tta   2120
Val Thr Gly Pro Gln Glu Ser Lys Ile Val Gly Ala Leu Glu Val Leu
        200                 205                 210

ggt aaa aaa gct gat atc gtc att gca aac caa aat ggt att acc tta   2168
Gly Lys Lys Ala Asp Ile Val Ile Ala Asn Gln Asn Gly Ile Thr Leu
215                 220                 225                 230

aat ggt gta aga aca ata aat tca gat cgt ttt gtt gcc act acg agt   2216
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40

```
Asn Gly Val Arg Thr Ile Asn Ser Asp Arg Phe Val Ala Thr Thr Ser
                235                 240                 245

gag ctt ata gat ccg aat cag atg atg tta aag gtt aca aaa gga aat    2264
Glu Leu Ile Asp Pro Asn Gln Met Met Leu Lys Val Thr Lys Gly Asn
                250                 255                 260

gtg atc att gat att gat ggt ttt tcg aca gat gga tta aag tat tta    2312
Val Ile Ile Asp Ile Asp Gly Phe Ser Thr Asp Gly Leu Lys Tyr Leu
                265                 270                 275

gat att att gct aaa aaa att gaa caa aag caa tca att aca tca ggg    2360
Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys Gln Ser Ile Thr Ser Gly
    280                 285                 290

gat aat tca gaa gca aaa aca gat gtc act ctt att gcg ggt tcc agt    2408
Asp Asn Ser Glu Ala Lys Thr Asp Val Thr Leu Ile Ala Gly Ser Ser
295                 300                 305                 310

gaa tat gat tta agc aaa cat gag ctg aaa aaa acg agc ggt gaa aat    2456
Glu Tyr Asp Leu Ser Lys His Glu Leu Lys Lys Thr Ser Gly Glu Asn
                315         .           320                 325

gta tct aat gat gtt att gct atc acg gga tct agt aca ggc gca atg    2504
Val Ser Asn Asp Val Ile Ala Ile Thr Gly Ser Ser Thr Gly Ala Met
                330                 335                 340

cat ggt aaa aat att aag ttg att gtg aca gat aaa ggt gca ggc gta    2552
His Gly Lys Asn Ile Lys Leu Ile Val Thr Asp Lys Gly Ala Gly Val
                345                 350                 355

aaa cat gat gga att att ttg tct gaa aat gat att cag att gaa atg    2600
Lys His Asp Gly Ile Ile Leu Ser Glu Asn Asp Ile Gln Ile Glu Met
    360                 365                 370

aat gaa ggt gac tta gaa ctt ggc aat acg att cag caa aca gtg gta    2648
Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr Ile Gln Gln Thr Val Val
375                 380                 385                 390

aaa aaa gac cga aat att cga gcc aag aaa aaa att gaa gtg aaa aac    2696
Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys Lys Ile Glu Val Lys Asn
                395                 400                 405

gct aat cgt gtt ttt gtt ggt agt caa acg aaa tca gat gaa att tcg    2744
Ala Asn Arg Val Phe Val Gly Ser Gln Thr Lys Ser Asp Glu Ile Ser
                410                 415                 420

tta gag gcg aaa caa gtt aaa atc aga aaa aac gca gag att agg agt    2792
Leu Glu Ala Lys Gln Val Lys Ile Arg Lys Asn Ala Glu Ile Arg Ser
            425                 430                 435

acg aca caa gcc aaa atc gta gca aag ggt gcc ctg tct att gag caa    2840
Thr Thr Gln Ala Lys Ile Val Ala Lys Gly Ala Leu Ser Ile Glu Gln
    440                 445                 450

aat gcg aag ctc gtc gct aaa aag ata gat gtg gca aca gaa act cta    2888
Asn Ala Lys Leu Val Ala Lys Lys Ile Asp Val Ala Thr Glu Thr Leu
455                 460                 465                 470

act aat gct ggg cgt att tat ggt cga gag gtt aag ctt gac act aat    2936
Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu Val Lys Leu Asp Thr Asn
                475                 480                 485
```

41

```
aat ttg att aat gat aaa gaa att tat gct gaa cgg aaa ttg agt att    2984
Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala Glu Arg Lys Leu Ser Ile
            490             495             500

ttg acg aaa gga aaa gat ctt gaa att att caa gat aga tat ttg tct    3032
Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile Gln Asp Arg Tyr Leu Ser
            505             510             515

cca ctg atg cgc gta aaa agt agt gtc cgc ttt tta ggc tct ccg ttt    3080
Pro Leu Met Arg Val Lys Ser Ser Val Arg Phe Leu Gly Ser Pro Phe
            520             525             530

ttc tca ata tct ccg tcg atg ctc gca agc ctt agt gca cag ttt aag    3128
Phe Ser Ile Ser Pro Ser Met Leu Ala Ser Leu Ser Ala Gln Phe Lys
535             540             545             550

cct ggt ttt gtg aat aag gga ctc att gaa agt gcg ggg agt gca gaa    3176
Pro Gly Phe Val Asn Lys Gly Leu Ile Glu Ser Ala Gly Ser Ala Glu
            555             560             565

tta act ttt aaa gaa aaa acc agt ttt tta aca gag ggc aat aat ttt    3224
Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu Thr Glu Gly Asn Asn Phe
            570             575             580

att aga gct aaa gat gcg tta ac                                     3247
Ile Arg Ala Lys Asp Ala Leu
            585


<210> 18
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<212> PRT
<213> Pasteurella multocida

<400> 18
Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys
  1               5                  10                  15


Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser
            20                  25                  30

Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
            35                  40                  45

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
      50                  55                  60

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
 65                  70                  75                  80

Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
                  85                  90                  95

Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
            100                 105                 110

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
            115                 120                 125

Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
      130                 135                 140
```

42

```
Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
145                 150                 155                 160

Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
                165                 170                 175

Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
                180                 185                 190

Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
                195                 200                 205

Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
210                 215                 220

Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
225                 230                 235                 240

Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
                245                 250                 255

Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
                260                 265                 270

Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
                275                 280                 285

Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
                290                 295                 300

Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
305                 310                 315                 320

Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
                325                 330                 335

Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
                340                 345                 350

Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
                355                 360                 365

Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
370                 375                 380

Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
385                 390                 395                 400

Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
                405                 410                 415

Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
                420                 425                 430

Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
                435                 440                 445

Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
                450                 455                 460

Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
465                 470                 475                 480
```

43

```
Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
                485                 490             495

Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
            500                 505             510

Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
            515                 520             525

Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
        530             535             540

Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
545             550             555             560

Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
                565             570             575

Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu
                580             585
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<210> 19
<211> 3247
<212> DNA
<213> Pasteurella multocida

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<222> (1)..(1446)

<220>
<223> fhaC

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gtc gac ctt gcg ggt gaa aag gta tct cta aat ttt ggc gat atc att    48
Val Asp Leu Ala Gly Glu Lys Val Ser Leu Asn Phe Gly Asp Ile Ile
  1               5                  10                  15

cat gct tac caa aac cag ccc cta tca aca aaa gtt gtt ttt caa tta    96
His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu
                20                  25                  30

gtg aaa gat ttg acg gaa gtt tta tac cgt tct ggc tac gtg aca agt   144
Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser
            35                  40                  45

gca att ggt tta aaa aat tca aaa atc agc aat ggc gat ctt gaa ttt   192
Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe
        50                  55                  60

att gta ctg tgg gga aga act cgc gat ctg ttt gtg aat ggg gag aaa   240
Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys
65                  70                  75                  80

cca acc cgt ttt aga gat aaa aca atg tta tca gtc cta ccc aat tta   288
Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu
                85                  90                  95

atc gga aat cgc tta agt att cac gac att gac cag ttg atc gaa atc   336
Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile
                100                 105                 110
```

44

```
tta aat act acg aat aaa aaa gcc aca gtg aat gtg gtt gca agt gaa    384
Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu
        115             120             125

gaa aaa ggc agc tca aat cta aat att gaa aga caa tat gat gtt ttt    432
Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe
    130             135             140

ccg caa gtg agt gtc gga ttc aat aat tca ggt gct ggc aat aat gcc    480
Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala
145             150             155             160

aat ggg cgt aat caa gct aca ttg aat att gct tgg agt gat cta tta    528
Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu
                165             170             175

ggc acg aat gat cgt tgg agt ttc tcg agt agt tac cgt tta tat aaa    576
Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys
            180             185             190

aat cat cat gct aac cag caa cgc aat tat act ttg tct tac agt cag    624
Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln
        195             200             205

cct ata ggc ttt tct aca gta gaa att aaa gca tcg gaa tct acg tat    672
Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr
    210             215             220

gaa aaa gaa ctt cgc ggt ata aat act cat tct tct cat ggg aaa acc    720
Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr
225             230             235             240

caa agc tta gct gtc aag ctg atg cat gtg tta ttg cgt aat aag gag    768
Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu
                245             250             255

agt att tta tct aca tat acc gag ttc gag ttt aaa aaa cgg att agt    816
Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser
            260             265             270

tat ttt tct gat att ttg att ggg aaa tat cac aat aat aaa gtg agc    864
Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser
        275             280             285

gta ggg tta tct tac atg act aat ttt gct tac ggg aag ctt tac agc    912
Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser
    290             295             300

gac att gct tac gcg aat ggg ttg aga tgg ttt ggg gcg aat tat tca    960
Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser
305             310             315             320

gca tat gat gca aat cgt gaa aaa acc tta aaa tta ttg tca gga agt   1008
Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser
                325             330             335

att aat tgg cag cgt cca ata tcc ctg ttt gaa cgt gcg atg aat tat   1056
Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr
            340             345             350

caa tta cgt att ggt gcc caa tat ggt ttt gat agt ttg tat tct gaa   1104
Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu
```

45

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aat caa ttt tca att ggt gat gaa tat aca gta aga gga ttt aaa ggt    1152
Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly
    370                 375                 380

ggt gcg gtt tct ggt gat agt ggt gcg tat tta tca caa aca ctg acg    1200
Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr
385                 390                 395                 400

gtt cct ttt tat cca caa aaa gca tat tta tct cag gta tcc cct ttt    1248
Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe
                405                 410                 415

att gga ttt gat atg ggt aaa gta cat att aaa tca aag cat aaa aca    1296
Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr
                420                 425                 430

acc act tta gtc ggt ttt gcc cta ggc ttg aaa acg caa ata aag tta    1344
Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu
                435                 440                 445

ttt tca tta tca tta acc tat gca caa cca atg aat ggt gtg agt ggt    1392
Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly
    450                 455                 460

gtt acg caa cat cgt caa aaa ccg att tat tat ttc tca gga tca ctt    1440
Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu
465                 470                 475                 480

tct ttt taatctcttt taagtttaag gattaactta atatgaacaa aaatcgttac    1496
Ser Phe

aaactcattt ttagtcaagt caaaggttgt ctcgttcctg tggcagaatg tattaactca   1556

gctattagca atggttcatc tgattcaaca tccacatcag aacaagttga agaggaacct   1616

ttccttctag aacaatattc actttcctcc gtgtctttat tagtaaaaag cacgttcaat   1676

cctgtttcgt atgcaatgca attgacttgg aaacagcttt ctattttatt tttaactgtg   1736

atttctgttc ctgttttggc tgagggaaaa ggggatgaaa gaaatcaatt aacagtgatt   1796

gataatagcg atcatattaa attagatgca tctaatcttg ctggtaatga taaaacaaaa   1856

atctatcaag cagaaaataa agttctggtt attgatattg ctaaaccaaa tgggaaaggg   1916

atttcagata accgttttga aaaatttaat attccaaata gcgcggtgtt taataataat   1976

gggactgaag cgcaggcaag atcaacatta attggttaca ttccgcaaaa tcaaaattta   2036

aggggaggga agaagctga tgttatatta aatcaagtga caggtcctca agaaagtaaa   2096

attgttggcg cgcttgaagt attaggtaaa aaagctgata tcgtcattgc aaaccaaaat   2156

ggtattacct taaatggtgt aagaacaata aattcagatc gttttgttgc cactacgagt   2216

gagcttatag atccgaatca gatgatgtta aaggttacaa aaggaaatgt gatcattgat   2276

attgatggtt tttcgacaga tggattaaag tatttagata ttattgctaa aaaaattgaa   2336

caaaagcaat caattacatc aggggataat tcagaagcaa aaacagatgt cactcttatt   2396
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gcgggttcca gtgaatatga tttaagcaaa catgagctga aaaaaacgag cggtgaaaat 2456

gtatctaatg atgttattgc tatcacggga tctagtacag gcgcaatgca tggtaaaaat 2516

attaagttga ttgtgacaga taaaggtgca ggcgtaaaac atgatggaat tattttgtct 2576

gaaaatgata ttcagattga aatgaatgaa ggtgacttag aacttggcaa tacgattcag 2636

caaacagtgg taaaaaaaga ccgaaatatt cgagccaaga aaaaaattga agtgaaaaac 2696

gctaatcgtg tttttgttgg tagtcaaacg aaatcagatg aaatttcgtt agaggcgaaa 2756

caagttaaaa tcagaaaaaa cgcagagatt aggagtacga cacaagccaa aatcgtagca 2816

aagggtgccc tgtctattga gcaaaatgcg aagctcgtcg ctaaaaagat agatgtggca 2876

acagaaactc taactaatgc tgggcgtatt tatggtcgag aggttaagct tgacactaat 2936

aatttgatta atgataaaga aatttatgct gaacggaaat tgagtatttt gacgaaagga 2996

aaagatcttg aaattattca agatagatat ttgtctccac tgatgcgcgt aaaaagtagt 3056

gtccgctttt taggctctcc gtttttctca atatctccgt cgatgctcgc aagccttagt 3116

gcacagttta agcctggttt tgtgaataag ggactcattg aaagtgcggg gagtgcagaa 3176

ttaacttttta aagaaaaaac cagttttttta acagagggca ataattttat tagagctaaa 3236

gatgcgttaa c                                                     3247


<210> 20
<211> 482
<212> PRT
<213> Pasteurella multocida

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Val Asp Leu Ala Gly Glu Lys Val Ser Leu Asn Phe Gly Asp Ile Ile
1               5                   10                  15


His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu
            20                  25                  30


Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser
        35                  40                  45


Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe
    50                  55                  60


Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys
65                  70                  75                  80


Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu
                85                  90                  95


Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile
            100                 105                 110


Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu
        115                 120                 125
```

47

```
Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe
130                 135                 140

Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala
145                 150                 155                 160

Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu
                165                 170                 175

Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys
            180                 185                 190

Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln
        195                 200                 205

Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr
    210                 215                 220

Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr
225                 230                 235                 240

Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu
                245                 250                 255

Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser
            260                 265                 270

Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser
        275                 280                 285

Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser
    290                 295                 300

Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser
305                 310                 315                 320

Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser
                325                 330                 335

Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr
            340                 345                 350

Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu
        355                 360                 365

Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly
    370                 375                 380

Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr
385                 390                 395                 400

Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe
                405                 410                 415

Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr
            420                 425                 430

Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu
        435                 440                 445

Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly
    450                 455                 460
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48

```
Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu
465                 470             475                 480

Ser Phe


<210> 21
<211> 1170
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (639)..(1022)

<220>
<223> greA

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aagcgttggg atcgcgcgaa ttgcgttgac cactggtgag atcggggtca cctgtaaaac 120

gtacgataag atcgccatgc atttcattgt tttttatttt tccattggtt aatagactgg 180

tttcaaattg aaattggtca cttagtacga gtttggcggt taaggcggtg agcacttttt 240

gtgtactggc gggtaacata aaggtactgg cttggtgcgc tacaattttt tcattacgat 300

ttaagttttt agccacaaaa cctaggctgg tcccttcggg taaatgagcg ttgatttcag 360

caagatcaat ctcagcataa ctgaaatgac tgacgagtaa actacatata agtatcgttc 420

gtttgaaaag gcgtaaaagc gtggcagtaa aaaaagaaga tattttatac ataattggct 480

cgagcagttg ctattttttt attgtcgaac aataatagta tttgaaccct cgagagtaaa 540

tcctttctc gttaaacact tatttttta ttcaactacg gcattgtttt tacaatgttg 600


tggtttgtt tttatctaaa aaggaagaaa aaacgatt atg aaa cag att cca atg 656
                                            Met Lys Gln Ile Pro Met
                                              1                   5

act ata cgt ggt gcg gaa caa tta aga caa gaa ctc gat ttt ttg aaa   704
Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln Glu Leu Asp Phe Leu Lys
             10              15                  20

aac act cgt cgc cca gaa att att aat gct atc gca gaa gct cgt gaa   752
Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala Ile Ala Glu Ala Arg Glu
         25              30              35

cat ggc gat cta aaa gaa aat gca gaa tac cat gct gcg cgt gaa cag   800
His Gly Asp Leu Lys Glu Asn Ala Glu Tyr His Ala Ala Arg Glu Gln
         40              45              50

caa gga ttt tgt gaa gga cga atc caa gaa att gaa ggg aaa tta gcg   848
Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu Ile Glu Gly Lys Leu Ala
  55              60              65                  70
```

49

```
aat agt caa att att gat gtc aca aag atc cca aat aat ggc aaa gtg    896
Asn Ser Gln Ile Ile Asp Val Thr Lys Ile Pro Asn Asn Gly Lys Val
                75                  80                  85

att ttt ggt gcc aca att ttg tta ctg aat att gac acg gaa gaa gaa    944
Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn Ile Asp Thr Glu Glu Glu
                90                  95                  100

gtc tcg tac caa att gta ggc gat gat gaa gcc aat att aaa gca ggg    992
Val Ser Tyr Gln Ile Val Gly Asp Asp Glu Ala Asn Ile Lys Ala Gly
            105                 110                 115

cta att tca gtt aac gcc acg cga ttg aat tagagaaagc taaatggatt     1042
Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
        120                 125

gcccaagatc ttggcgtcaa acaaacgtta attgacactt ccgtcattaa agcgattacg 1102

caaaatgcct taatggacga acaggcaaga attgagcaac atggcagtac accgaatact 1162

ttcgttga                                                          1170


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<212> PRT
<213> Pasteurella multocida

<400> 22
Met Lys Gln Ile Pro Met Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln
 1               5                  10                  15

Glu Leu Asp Phe Leu Lys Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala
            20                  25                  30

Ile Ala Glu Ala Arg Glu His Gly Asp Leu Lys Glu Asn Ala Glu Tyr
        35                  40                  45

His Ala Ala Arg Glu Gln Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu
    50                  55                  60

Ile Glu Gly Lys Leu Ala Asn Ser Gln Ile Ile Asp Val Thr Lys Ile
65                  70                  75                  80

Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
                85                  90                  95

Ile Asp Thr Glu Glu Glu Val Ser Tyr Gln Ile Val Gly Asp Asp Glu
            100                 105                 110

Ala Asn Ile Lys Ala Gly Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
        115                 120                 125


<210> 23
<211> 4666
<212> DNA
<213> Pasteurella multocida

<220>
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<222> (980)..(2440)
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50

<220>
<223> guaB

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tcatcaattc ctgcttgttc aaaatgttgt aaacgtgcaa tcaacttttt acctaattct 120

gcgatcaatt tattccgatc aatcgttggt aatacttcaa tcagctctgc ccaaggttga 180

tcaatttgct gtgtttgttt tgggaaagac aaattaatgc caaagccaat cacgagatta 240

tgttgattat tctgacgatt ggcgatttcg accaaaatcc ctgctaattt gcgcccatgt 300

aatagcacat catttggcca ttttaatcca atgttcaaag cacctgcttg ctttagcgtt 360

tctgcgattg ccatacccac tactaaactc aagccttcta aattgacctt ttggtcacat 420

gcccaataca aactcataat cacttgtcca gcaaaaggag aaagccattg acgaccacgt 480

cgtccacgtc ccgcagtttg atattctgct aagcaaatag cgcctttttc caaatgtgca 540

atattgtcaa gcaagaattg attggtcgag ttaataatcg gcttaatata aagtgggtaa 600

ggtgctaacg cttgcgtcaa ataagattca tttaagcgac ttaattgagg tatgagacga 660

aaatgttgga cttgctgttc tatttgtatc ccttgttgtt tcaatttttc gatattgtgt 720

aagatatctt gttctgaata acctaaaagt gcagtcaatt ctgctaaaga aagttgttga 780

tagctagcga gtaatgcaag tacgttttgc ataaaaatcc ttatttatat aaccaaagag 840

aggcaactta ttatagacaa tgattttctc gaaatcgat aaaaaaatcc attttcaaac 900

agcaacgaaa tctgtataat gcgaccgcaa tattttttac ccttttattt ttcatatcaa 960

cctaagagag aatattgca atg tta cga gta ata aaa gaa gca tta acc ttc 1012
                          Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe
                          1   5   10

gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc 1060
Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr
            15   20   25

gca gac ctt tcc act caa ctc acc aaa act atc cgc ctc aat atc cca 1108
Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro
        30   35   40

atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc 1156
Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile
    45   50   55

tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct 1204
Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser
60   65   70   75

att gag cgt caa gcg gaa cgt gtc cgc aaa gtg aaa aaa ttt gag agc 1252
Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser
                80   85   90

ggt att gta tcc gat cct gtc acc gtt tca cca acc tta tct tta gca 1300
Gly Ile Val Ser Asp Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala

51

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                    95                        100                        105
     gaa tta agt gaa tta gtg aag aaa aat ggt ttt gcg agt ttc cct gtt      1348
     Glu Leu Ser Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val
             110                 115                 120

     gtt gat gat gaa aaa aat ctt gtc ggt atc att act ggt cgt gat aca      1396
     Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr
         125                 130                 135

     cgc ttt gtc acg gat tta aat aaa aca gtg gcg gac ttt atg acc cct      1444
     Arg Phe Val Thr Asp Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro
     140                 145                 150                 155

     aaa gct cgt ctt gtc acg gtg aaa cgc aat gca agt cgc gat gaa att      1492
     Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile
                 160                 165                 170

     ttt ggt cta atg cat aca cac cgt gta gaa aaa gtc ctt gtt gtc agc      1540
     Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Val Ser
                 175                 180                 185

     gac gat ttc aaa tta aaa ggc atg atc acc tta aaa gac tac caa aaa      1588
     Asp Asp Phe Lys Leu Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys
                 190                 195                 200

     tcc gag caa aaa cca caa gcc tgt aaa gat gaa ttt ggt cgt tta cgt      1636
     Ser Glu Gln Lys Pro Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg
             205                 210                 215

     gtc ggt gct gca gta gga gca gga cct ggt aat gaa gaa cgt att gat      1684
     Val Gly Ala Ala Val Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp
     220                 225                 230                 235

     gca tta gtg aaa gca ggg gtc gat gtg tta ttg att gac tca tca cac      1732
     Ala Leu Val Lys Ala Gly Val Asp Val Leu Leu Ile Asp Ser Ser His
                 240                 245                 250

     ggt cat tca gaa ggt gtg tta caa cgt gtg cgt gaa act cgt gcg aaa      1780
     Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys
                 255                 260                 265

     tac cca gat ttg cca att gtt gca ggt aat gtg gca acc gct gaa ggc      1828
     Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly
                 270                 275                 280

     gca att gcg ttg gct gat gca ggg gca agt gca gtg aaa gtg ggg att      1876
     Ala Ile Ala Leu Ala Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile
             285                 290                 295

     ggt cct ggt tca att tgt aca aca cgt att gtc aca ggc gtg ggc gtt      1924
     Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val
     300                 305                 310                 315

     cca caa att aca gcg att gcc gat gcg gca gaa gca cta aaa gat cgg      1972
     Pro Gln Ile Thr Ala Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg
                 320                 325                 330

     ggt att cct gtg att gca gat ggc ggt atc cgt ttc tct ggt gat att      2020
     Gly Ile Pro Val Ile Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile
                 335                 340                 345
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52

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tcg aaa gcc att gcg gcg ggc gcc tct tgt gtt atg gtg ggt tcc atg    2068
Ser Lys Ala Ile Ala Ala Gly Ala Ser Cys Val Met Val Gly Ser Met
        350             355             360

ttt gca ggt aca gaa gaa gca cca ggt gaa atc gaa ctt tat caa ggt    2116
Phe Ala Gly Thr Glu Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly
    365             370             375

cgt gcc ttt aaa tct tat cga ggt atg gga tcg tta ggt gcg atg agc    2164
Arg Ala Phe Lys Ser Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser
380             385             390             395

aaa ggc tca agc gac cgc tat ttc cag tcc gat aat gca gct gac aaa    2212
Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys
                400             405             410

tta gta cca gaa ggt att gaa gga cgt att cca tat aaa gga ttc tta    2260
Leu Val Pro Glu Gly Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu
                415             420             425

aaa gaa att atc cat caa caa atg ggt gga ttg cgt tct tgt atg ggc    2308
Lys Glu Ile Ile His Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly
            430             435             440

tta acg ggt tgt gca acc att gat gaa ctc cgt acc aaa gcg cag ttt    2356
Leu Thr Gly Cys Ala Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe
        445             450             455

gtg cgc att agt ggt gca ggg atc caa gaa agc cat gtg cat gat gtg    2404
Val Arg Ile Ser Gly Ala Gly Ile Gln Glu Ser His Val His Asp Val
460             465             470             475

act atc aca aaa gaa gcc cct aat tat cgt atg ggt taaacattgc         2450
Thr Ile Thr Lys Glu Ala Pro Asn Tyr Arg Met Gly
            480             485

ttaggtgggg attatcccca cctaagttta ttttaaataa caacgttaat agagaagctt 2510

atttttatgt atggcattaa aattaaaaat gttattaaac tttttctatt aaagttttta 2570

agaaataaat atcgatataa aatcaatatt caacatcatc tcattagtat tgaaggaaaa 2630

tgcggtgagt ttgatttaag ccagctaaac tatgtttatt tggtgaaaga tcctgagata 2690

agaaataatc gactgacact gtacttgaat gatttttttca aaattggggt aaattatcat 2750

ggatttactc aaatgtatca gacactatca tccaagtatg gttttgatga cgcaacgttt 2810

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caaaattatg tgattcttga tgaagcctat actgactata cacaaggttt tgaaattcaa 2930

tctcctgaaa aaatatttat tccttggggg actacttatg aagccttatt tcagcagaca 2990

caatttaaag aaaaaggaat ctcttatgac tttatcttcc ctattcggat agggcgttta 3050

ttactcaagg atgtgtggat cacaccaagt gtccgaaaag atgtaccgat tttagcgtta 3110

tacactgagt gctatcatga atccgcgaca gaaaaaagtt atcaggaatt aaccgccgca 3170

ttacgtgaga accaacagtt aatcagatca tgtgttgaag aacgagccga tccgaaatta 3230
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53

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tataagtctg ttttacgcct taacgcgaca gaatttgaat tgcgttatta tcgacatata 3290

cgagacgatt ttgatagggg atacactaaa ttcagcatta gagatacgac agactattta 3350

gattatgtga tcaacgagcc ttatgaaaat caattagtga taacggatta tttagtgatt 3410

gaggcgcaaa atttaataaa aatggattat accgataatt ccattattaa acgccgacca 3470

ccaaaaataa aagaaaagtt tcgtgatgca caaagcctga tttggacaga tgatctcaat 3530

cataaaatcg gttttaccag tgatgaccgc gctatcgtct ttgataaagc ggacattgaa 3590

tcctttactc tggcaaatat agagacaacc cgaagacata atcgcagttc actcagcatc 3650

tgttttgtgg ataaaaataa ggaagccatc actgtatttc tagctgaaca tcattttctg 3710

ataccctatg tggataaaat aaaaacactg acacaaaaag aggtgttgtt tcttgaagaa 3770

tatatagagg atgtttaaaa aaccgataac atcttgatgt catcgcaaat tcaaactcct 3830

tttacacaat atatttaaac tttaacccga tttaatattt acgtaaaaac aactaagaga 3890

acttaaatga acaacattca caaccataaa attttaattt tggacttcgg ttcacaatat 3950

acccagttga ttgcccgccg tgtacgtgaa attggcgtgt actgcgaact ttgggcatgg 4010

gatgtatccg aagccgatat tcgtgagttt aatccaactg ggattattct ttctggtggt 4070

cctgaaagta ccactgaaga aaacagccca cgagctcccg aatacgtatt caacgccggt 4130

gtacccgtat tagggatctg ttatggtatg caaaccatgg cgatgcaact aggtggttta 4190

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gcgttatttg ctcaattaaa tgatgatgtc gcaagttcac agcccaaatt agacgtttgg 4310

atgagccatg gcgataaagt gacgcgtttg ccagatcatt ccaagtcac cgcaatgacc 4370

tcaacctgtc caatcgcagc tatgtcggat gaacgtcgtc gtttttatgg tgtccaattc 4430

cacccagaag tgactcatac aaaaagcggg cttgaattat taacgaattt tgtggtgaag 4490

atctgtggtt gtgaacgtaa ctggacacca gaaaatatca ttgaagatgc cgttgctcgt 4550

cttaaagcac aagtgggcga tgatgaagtg attttaggct tatctggtgg cgttaactgc 4610

cgtataggca gcttagaaaa agtgtccgcg ctcacgttaa tccccgtaag cgttga      4666
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<400> 24
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Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe Asp Asp Val Leu Leu
 1               5                  10                  15

Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
            20                  25                  30

Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
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54

Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
    50   55   60

Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
65   70   75   80

Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Asp
          85   90   95

Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala Glu Leu Ser Glu Leu
       100   105   110

Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val Val Asp Asp Glu Lys
    115   120   125

Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
    130   135   140

Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro Lys Ala Arg Leu Val
145   150   155   160

Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile Phe Gly Leu Met His
        165   170   175

Thr His Arg Val Glu Lys Val Leu Val Val Ser Asp Asp Phe Lys Leu
        180   185   190

Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ser Glu Gln Lys Pro
    195   200   205

Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
    210   215   220

Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
225   230   235   240

Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
        245   250   255

Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
        260   265   270

Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
    275   280   285

Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
    290   295   300

Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala
305   310   315   320

Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg Gly Ile Pro Val Ile
        325   330   335

Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile Ser Lys Ala Ile Ala
        340   345   350

Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu
    355   360   365

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Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser
    370             375             380

Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp
385             390             395             400

Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly
            405             410             415

Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu Lys Glu Ile Ile His
            420             425             430

Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
            435             440             445

Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly
        450             455             460

Ala Gly Ile Gln Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu
465             470             475             480

Ala Pro Asn Tyr Arg Met Gly
                485


<210> 25
<211> 2364
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (191)..(1828)

<220>
<223> Hi1501

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tgcgctagag atgctgtgga aaaatgcggt aagcagctct gccccgattg agttcatgac 120

aattgacggc gatttagggc gtgatgaatt tgatgacggc gatttataca gtatttggcg 180

gagataaaaa atg gcg aag aaa aag aaa aaa tta caa caa gcg aaa aaa 229
            Met Ala Lys Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys
             1               5                  10

gta caa gtt ggc tta gat aca caa aca aat gag gcg cgt gtc acg gag 277
Val Gln Val Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu
     15              20              25

aca gga aga att att tct gat cac cca agc aat aaa att acc ccc gca 325
Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala
 30              35              40              45

aag tta aaa ggg att tta gaa gat gct gaa ggt ggt gat att acc gcg 373
Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala
             50              55              60

caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg 421
Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly
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56

gca aat att caa acc cgt aag cgt gcg att tta acc ctt gac tgg cgc   469
Ala Asn Ile Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg
            80   85   90

att gca gag cca cgt aat gcc aca ccg caa gaa gaa aaa ctg caa gtc   517
Ile Ala Glu Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val
        95   100   105

gaa att gac gag ctt ttc tat caa ttc cca atg cta gaa gat tta atg   565
Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met
110   115   120   125

gtg gat atg atg gat gcg gta gga cat ggt ttt tcg gcg tta gaa att   613
Val Asp Met Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile
                    130   135   140

gaa tgg aag caa gct gaa agt aaa tgg att cca gtt aat ttt atc gca   661
Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala
                145   150   155

cgt ccg cag tcg tgg ttt aaa cta gac aag gat gat aat tta ctg ctt   709
Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu
            160   165   170

aaa acg cca gat aat caa gac ggt gag ccg ttg aga caa tat ggc tgg   757
Lys Thr Pro Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp
        175   180   185

gta gtg cat acc cac aaa tca aga aca gta cag ctt gct cgt atg ggt   805
Val Val His Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly
190   195   200   205

tta ttt aga acg ctc gca tgg ctt tat atg ttt aaa cac tac tcg gtg   853
Leu Phe Arg Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val
                    210   215   220

cat gat ttt gcc gaa ttt cta gag ctt tat ggt atg ccg att cgt att   901
His Asp Phe Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile
                225   230   235

ggt aaa tac cca ttt ggg gca acg aat gac gaa aag cgc aca tta ttg   949
Gly Lys Tyr Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu
            240   245   250

cgt gca ctt gct caa atc gga cat aac gca gca ggg att atg cca gaa   997
Arg Ala Leu Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu
        255   260   265

gga atg aat gtt gag ttg cat aat gtg aca aac act act ggc tcg gct   1045
Gly Met Asn Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala
270   275   280   285

gga agc aac ccg ttt ttg caa atg gtg gac tgg tgt gaa aag tcc gcc   1093
Gly Ser Asn Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala
                290   295   300

gca cgt ttg att cta ggg caa aca tta aca agc ggt gca gat ggt aaa   1141
Ala Arg Leu Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys
                305   310   315

57

```
act tca act aat gcc ctt gga caa gtg cat aat gaa gtc aga cgt gac    1189
Thr Ser Thr Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp
        320             325                 330

ttg ctt gtg tct gat gct aaa cag att gca caa act att aca caa cag    1237
Leu Leu Val Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln
        335             340                 345

att att ctg cca tat ctt caa att aac att gat ccg aat att ttg cct    1285
Ile Ile Leu Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro
350             355             360                 365

tct cgt gtg ccg tat ttc gag ttt gac acg aaa gaa tat gct gat tta    1333
Ser Arg Val Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu
            370             375             380

agt gtc cta gcg gat gct att cct aag ctt gtg agc gta gga gtg cgc    1381
Ser Val Leu Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg
            385             390             395

att cct gaa aat tgg gtg cgt gat aaa gcg ggc att cca gaa ccg cag    1429
Ile Pro Glu Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln
        400             405                 410

gaa aat gaa acg att tta agt gcg gtt caa cat gat ttt aaa aca gat    1477
Glu Asn Glu Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp
        415             420                 425

tta aac gat gtt gaa aat ccg aaa aaa cag acc gca ctt tct gta caa    1525
Leu Asn Asp Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln
430             435             440                 445

aat cac gtg aca ggt tgt cag tgt gat ggc tgt cgt ggt gtt gca tta    1573
Asn His Val Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu
            450             455             460

tct gcg aat aat aac agt tct act gcg cag ggc gtg cta gat ggt gga    1621
Ser Ala Asn Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly
            465             470             475

ctt gcg caa gca ttt aat gag cct gat ttt aat aaa caa tta aat cca    1669
Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro
        480             485                 490

atg gta aag aaa gct gtt gcg gta ctc atg gca tgt gac tct tac gat    1717
Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp
        495             500                 505

gag gcg gca gaa aaa ctc gct gaa gca tac cca gaa att tca agt cac    1765
Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His
510             515             520                 525

gaa cac gaa cag tat ctc tca aat gcg ctg ttt tta gct gat tta ctt    1813
Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu
            530             535             540

gga gga act aat gtc taaaccgctt agttttctat tcggacttga accaacgcaa    1868
Gly Gly Thr Asn Val
            545


gccattgagt ttttacataa taaaaaatta cttgcaacga aagtgtttaa aaaatcactg 1928
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58

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catgatagtg ccatcgcaag agctacaaca atcgcgagat tatctagtct tgagatgacg 1988

aatgatattt ataaatcaat ggaagttgcc aaaaaagagg gtaagagctt tacacaatgg 2048

aaaaaagact tggtaagtga gtttgagaaa aaaggctggg tattcgggca tgataaatct 2108

atcagtcgcg gtatcgacgg aaaactgttg gctgatccga aaacaggcga atattttggt 2168

acaccgcgtc ggctgaatac aatttatcgt acaaacgtgc aagccgcata ttctgcggcg 2228

cgctatcagc gcatgatgga taatattgat catcgcccct attggcaata ttccgctgtc 2288

agcgatgagc gtacacgacc ctctcatctt gcactaaacg gtcgaattta tcgctatgat 2348

gacccgtttt ggtcga                                                  2364
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<210> 26
<211> 546
<212> PRT
<213> Pasteurella multocida

<400> 26

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Met Ala Lys Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys Val Gln Val
 1               5                  10                  15

Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu Thr Gly Arg
            20                  25                  30

Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala Lys Leu Lys
        35                  40                  45

Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala Gln His Glu
    50                  55                  60

Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly Ala Asn Ile
65                  70                  75                  80

Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg Ile Ala Glu
                85                  90                  95

Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val Glu Ile Asp
            100                 105                 110

Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met Val Asp Met
            115                 120                 125

Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile Glu Trp Lys
    130                 135                 140

Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala Arg Pro Gln
145                 150                 155                 160

Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu Lys Thr Pro
                165                 170                 175

Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp Val Val His
            180                 185                 190

Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly Leu Phe Arg
            195                 200                 205
```

59

Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val His Asp Phe
    210   215   220

Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile Gly Lys Tyr
225   230   235   240

Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu Arg Ala Leu
                245   250   255

Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu Gly Met Asn
                260   265   270

Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala Gly Ser Asn
                275   280   285

Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala Ala Arg Leu
    290   295   300

Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys Thr Ser Thr
305   310   315   320

Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp Leu Leu Val
                325   330   335

Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln Ile Ile Leu
                340   345   350

Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro Ser Arg Val
                355   360   365

Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu Ser Val Leu
    370   375   380

Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg Ile Pro Glu
385   390   395   400

Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln Glu Asn Glu
                405   410   415

Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp
                420   425   430

Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln Asn His Val
                435   440   445

Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu Ser Ala Asn
    450   455   460

Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly Leu Ala Gln
465   470   475   480

Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro Met Val Lys
                485   490   495

Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp Glu Ala Ala
                500   505   510

Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His Glu His Glu
                515   520   525

Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu Gly Gly Thr
    530   535   540

60

Asn Val
545

<210> 27
<211> 1353
<212> DNA
<213> Pasteurella multocida

<220>
<223> hmbR

<220>
<221> CDS
<222> (2)..(1351)

<400> 27
g tca acg aaa gtc ggt tac gat att aat aac act cat cgt ttt aca ctg 49
  Ser Thr Lys Val Gly Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu
    1   5   10   15

ttt tta gaa gat cgc cgt gaa aag aag ctt acc gaa gaa aaa aca tta 97
Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu
         20   25   30

ggg ctt agt gat gca gtg cgt ttt gct aat gat caa acc cct tat ctc 145
Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
         35   40   45

cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193
Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
         50   55   60

gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241
Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
65   70   75   80

caa gag ttt gat att aat aat agg aat aaa ttg gat tcg act atg tcg 289
Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
         85   90   95

ttt gta tat tta caa aga cag aat ata gct cgg gga gaa ttt tca acg 337
Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
         100   105   110

agt cct tta tat tgg ggg ccg agt cgc cat cgt tta tnt gcg aaa ttc 385
Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
         115   120   125

gaa ttt cgt gat ang ttt tta gaa aat atg aat aag cnt ttt acg ttt 433
Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
         130   135   140

cgg ccg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat 481
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr
145   150   155   160

aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg 529
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
         165   170   175

gac gac att aag att ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg 577

61

```
Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg
        180                     185             190

tgg gat cac tat aac tat aag cca tta tta aat tct cag cat aat atc    625
Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile
        195                 200             205

aac agg aca cag aga tta cct tat cca aaa aca tca tcc aaa ttt tcg    673
Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser
        210                 215             220

tat caa ttg agt tta gag tat caa tta cat cca tca cat caa att gca    721
Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala
225                     230             235                 240

tac cgt tta agt acc ggt ttt agg gtt ccc cgt gtt gaa gat ctt tat    769
Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr
                245             250             255

ttt gaa gac cga gga aaa agt tct tca caa ttt ctt cct aac ccc gat    817
Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp
                260             265             270

cta caa ccg gaa act gca ctg aat cat gaa ata agt tac cgt ttc caa    865
Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln
                275             280             285

aat caa tat gcc cat ttc agc gtc ggg ctt ttc cgt aca cgt tat cat    913
Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His
        290             295             300

aac ttt att caa gaa cgt gag atg acc tgt gat aaa att cca tat gag    961
Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu
305                     310             315                 320

tat aat agg act tat gga tat tgc acg cat aat act tat gta atg ttt   1009
Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe
                325             330             335

gtt aat gaa cct gaa gcc gtg att aaa ggg gtt gaa gta agc ggt gct   1057
Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala
                340             345             350

tta aat ggg tcg gca ttc gga ctt tcc gac ggt tta act ttc cgt ctc   1105
Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu
                355             360             365

aaa ggg agc tac agc aaa ggt caa aat cat gac ggc gat ccg tta aaa   1153
Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys
        370             375             380

tct att caa cca tgg aca gtg gta acc ggt att gat tac gaa act gaa   1201
Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu
385                     390             395                 400

ggg tgg agc gtg agt ttg agc ggg cgt tat agt gcg gct aaa aaa gcc   1249
Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
                405             410             415

aaa gat gcg ata gaa acg gaa tac aca cat gat aaa aag gtt gtc aaa   1297
Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys
                420             425             430
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62

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caa tgg ccg cat tta agt cca tcc tac ttt gtt gtt gat ttt acg ggg      1345
Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly
        435                 440                 445

caa gtt ga                                                            1353
Gln Val
    450


<210> 28
<211> 450
<212> PRT
<213> Pasteurella multocida

<400> 28
Ser Thr Lys Val Gly Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu
 1               5                  10                  15

Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu
            20                  25                  30

Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
        35                  40                  45

Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
    50                  55                  60

Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
65                  70                  75                  80

Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
                85                  90                  95

Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
            100                 105                 110

Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
        115                 120                 125

Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
    130                 135                 140

Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr
145                 150                 155                 160

Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
                165                 170                 175

Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg
            180                 185                 190

Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile
        195                 200                 205

Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser
    210                 215                 220

Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala
225                 230                 235                 240

Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr
                245                 250                 255
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63

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Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp
            260                 265                 270

Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln
            275                 280                 285

Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His
            290                 295                 300

Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu
305                 310                 315                 320

Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe
                325                 330                 335

Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala
            340                 345                 350

Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu
            355                 360                 365

Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys
            370                 375                 380

Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu
385                 390                 395                 400

Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
                405                 410                 415

Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys
                420                 425                 430

Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly
            435                 440                 445

Gln Val
    450


<210> 29
<211> 4936
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1078)..(2769)

<220>
<223> hxuC

<400> 29
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ccgatttaac gcaaattaat gccgtcaaca ttcatctttt cctatcataa agcgtttcat 120

catggctagc attctagcaa aaattagttg aggaaaatag cggtcttgtt ttgcttaaaa 180

aacaacccac cccgtagggc acggctgttt cttttgaga aattacgctt cttcatcttg 240

atctttttc aagatctcat cttcattgag ttttaaaga cgggcaatcg cattgcggta 300
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64

ggagatttca aggctttctc gactagtagc aatgacacct tgatcgatta agaaaccgtc 360

attgacatca taaacccaac catgtaatga gagttttttc ccatttttcc acgcggattt 420

aatgattgac gagcgaccta agttataaac ttgctctgcg acgttaattt tcgtcagcat 480

atcagcccgt ttttcaggcg gtaaattgcc aagtaaatga ctatgcttat accaaatatc 540

gcgtaagtgg agtaaccagt tattaattaa acctaaatct tgatccgcca ttgcggcttt 600

aattccacca cagtttgtat gtccacaaat aataatgtgt tcaatattta agacctcaac 660

ggcatattgc acaacagata aacagtttaa atcggtgtga atgacttgat ttgcaacatt 720

acgatgcaca aacagctcac ccggtcctaa atttgttaat ttttctgcag gaacacggct 780

atccgagcaa ccaatccaaa gatagctcgg ggtttgatga tcagccaatt ctttaaagta 840

agaggagttt tcctctttca tccgtaacgc ccagctataa ttattggcaa aaagttgttc 900

aatttttttc attagagtga ttcctatacc gcaaaaataa gggggctagt atagcttaga 960

aatagacagt gggtaaagaa aggcaaaaaa ttgtatagga taacttgttt tttattgcca 1020

tttatttaga attagaatct ttaataataa aaataattat cattaaggtt aatagtt 1077

atg gat aaa aat tta atg aag gga tgt gta ttc tta tca ata gtc ggt 1125
Met Asp Lys Asn Leu Met Lys Gly Cys Val Phe Leu Ser Ile Val Gly
 1   5   10   15

tgc ggt atc caa ata ggg cta gca tca aat cca aat cct cca gat gtg 1173
Cys Gly Ile Gln Ile Gly Leu Ala Ser Asn Pro Asn Pro Pro Asp Val
             20   25   30

gat gag tta tta cct att att gtg aat gct gat gaa gat aat aaa tta 1221
Asp Glu Leu Leu Pro Ile Ile Val Asn Ala Asp Glu Asp Asn Lys Leu
         35   40   45

cca ggt cgt tct gta tta aaa cag aaa aat atc gat caa caa caa gca 1269
Pro Gly Arg Ser Val Leu Lys Gln Lys Asn Ile Asp Gln Gln Gln Ala
     50   55   60

gat aat gcc gct gac tta ata aat att tta cct ggg gta aat atg gcg 1317
Asp Asn Ala Ala Asp Leu Ile Asn Ile Leu Pro Gly Val Asn Met Ala
65   70   75   80

gga gga ttt cgc cct ggt ggt caa aca tta aat att aat gga atg ggt 1365
Gly Gly Phe Arg Pro Gly Gly Gln Thr Leu Asn Ile Asn Gly Met Gly
             85   90   95

gat gct gaa gat gtt aga gtt caa cta gac ggc gca aca aaa agt ttc 1413
Asp Ala Glu Asp Val Arg Val Gln Leu Asp Gly Ala Thr Lys Ser Phe
             100   105   110

gaa aaa tat caa caa ggc tct att ttt att gaa cct gag tta tta aga 1461
Glu Lys Tyr Gln Gln Gly Ser Ile Phe Ile Glu Pro Glu Leu Leu Arg
             115   120   125

aag gtg aca gta gac aaa gga aat tat tct cct caa tat ggc aat ggt 1509
Lys Val Thr Val Asp Lys Gly Asn Tyr Ser Pro Gln Tyr Gly Asn Gly
     130   135   140

65

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ggc ttt gct ggt act gta aaa ttt gaa aca aaa gat gca act gat ttt    1557
Gly Phe Ala Gly Thr Val Lys Phe Glu Thr Lys Asp Ala Thr Asp Phe
145             150             155                 160

ttg aaa gaa aat cag aaa ata ggt gga tta ttt aaa tat gga aat aat    1605
Leu Lys Glu Asn Gln Lys Ile Gly Gly Leu Phe Lys Tyr Gly Asn Asn
                165             170                 175

agc aat aat aac caa aaa act tat agt aca gcc cta gtt tta cag aat    1653
Ser Asn Asn Asn Gln Lys Thr Tyr Ser Thr Ala Leu Val Leu Gln Asn
            180             185             190

gaa caa aaa aat att gat ttg tta tta ttt ggt tct gta aga aat gca    1701
Glu Gln Lys Asn Ile Asp Leu Leu Leu Phe Gly Ser Val Arg Asn Ala
            195             200             205

agc aat tat aca aga cct gat aaa agt aaa att ctt ttt tca aaa aac    1749
Ser Asn Tyr Thr Arg Pro Asp Lys Ser Lys Ile Leu Phe Ser Lys Asn
    210             215             220

aat caa aaa agt gga tta ata aaa gta aat tgg caa att act cct gaa    1797
Asn Gln Lys Ser Gly Leu Ile Lys Val Asn Trp Gln Ile Thr Pro Glu
225             230             235             240

cat tta tta act tta tcc agt gtt tat ggc att cat aaa ggg tgg gaa    1845
His Leu Leu Thr Leu Ser Ser Val Tyr Gly Ile His Lys Gly Trp Glu
                245             250             255

cct tgg gca gca aaa aga gat gtg atg tcg aga cca aca gaa aca gaa    1893
Pro Trp Ala Ala Lys Arg Asp Val Met Ser Arg Pro Thr Glu Thr Glu
            260             265             270

ata aaa cac tat ggg att gat gtt gcg tgg aaa cgt aaa ctt gtt tat    1941
Ile Lys His Tyr Gly Ile Asp Val Ala Trp Lys Arg Lys Leu Val Tyr
            275             280             285

cga gat caa aaa gat gaa agt tat tca ttg aaa tat cgc tat tta cct    1989
Arg Asp Gln Lys Asp Glu Ser Tyr Ser Leu Lys Tyr Arg Tyr Leu Pro
    290             295             300

gaa aat aat aag tgg att aat ttg tct gtt cag ctg agt tat agt aaa    2037
Glu Asn Asn Lys Trp Ile Asn Leu Ser Val Gln Leu Ser Tyr Ser Lys
305             310             315             320

aca gag cag aat gat act cgc cat gag aaa gtc act tct tca ttc cta    2085
Thr Glu Gln Asn Asp Thr Arg His Glu Lys Val Thr Ser Ser Phe Leu
            325             330             335

ggt aca tta gga aat aaa agt tgg ata act tat tca gat ctt act ttt    2133
Gly Thr Leu Gly Asn Lys Ser Trp Ile Thr Tyr Ser Asp Leu Thr Phe
            340             345             350

gat ata agt aac aca agt act cta aat att ggg cgt gct gag cat gaa    2181
Asp Ile Ser Asn Thr Ser Thr Leu Asn Ile Gly Arg Ala Glu His Glu
            355             360             365

cta cta ttt ggt tta cag tgg tta aaa aat aaa aga aat acc ctt atg    2229
Leu Leu Phe Gly Leu Gln Trp Leu Lys Asn Lys Arg Asn Thr Leu Met
    370             375             380

tat cat aaa ggg gga gtc aag aag gca gac tat aat tat ggc tat ttt    2277
Tyr His Lys Gly Gly Val Lys Lys Ala Asp Tyr Asn Tyr Gly Tyr Phe
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66

cag cct tat tat atg cct tct gga cgc cag tat aca caa gca ttt tat   2325
Gln Pro Tyr Tyr Met Pro Ser Gly Arg Gln Tyr Thr Gln Ala Phe Tyr
                405   410   415

tta caa gat caa ata aaa tgg cag aat ttc ctc ttt aca gga ggg ata   2373
Leu Gln Asp Gln Ile Lys Trp Gln Asn Phe Leu Phe Thr Gly Gly Ile
                420   425   430

aga tat gac cat atc aat aat ata ggg cag aaa aat tta gcg cca cga   2421
Arg Tyr Asp His Ile Asn Asn Ile Gly Gln Lys Asn Leu Ala Pro Arg
            435   440   445

tat aat gat atc tct gca gga cat gat tat agc cag aaa aat tat aat   2469
Tyr Asn Asp Ile Ser Ala Gly His Asp Tyr Ser Gln Lys Asn Tyr Asn
        450   455   460

ggt tgg tct tat tat tta ggt ctt aag tat gat gta aat cat tat tta   2517
Gly Trp Ser Tyr Tyr Leu Gly Leu Lys Tyr Asp Val Asn His Tyr Leu
465   470   475   480

agt tta ttt acg aat ttt agt aaa act tgg cga gcc cct gtt att gat   2565
Ser Leu Phe Thr Asn Phe Ser Lys Thr Trp Arg Ala Pro Val Ile Asp
                485   490   495

gaa cag tat gag aca caa tat agt caa gct tct gta tct gcg act tct   2613
Glu Gln Tyr Glu Thr Gln Tyr Ser Gln Ala Ser Val Ser Ala Thr Ser
                500   505   510

tta aat tta gaa aaa gaa atg att aat caa acc aga gtg ggt gga att   2661
Leu Asn Leu Glu Lys Glu Met Ile Asn Gln Thr Arg Val Gly Gly Ile
                515   520   525

att act ctc aat cat cta ttt cag gaa aat gat gct ttt caa ttt aga   2709
Ile Thr Leu Asn His Leu Phe Gln Glu Asn Asp Ala Phe Gln Phe Arg
        530   535   540

act act tat ttt tac aat cgc ggc aag aat gaa atc ttc aaa acg aga   2757
Thr Thr Tyr Phe Tyr Asn Arg Gly Lys Asn Glu Ile Phe Lys Thr Arg
545   550   555   560

ggg gtt aac cgt tagagttggt tgaaatgact gaaaaattag acctatacgt   2809
Gly Val Asn Arg

tactgttaaa ggtggcggta tttctggtca agcgggtgca atccgtcacg gtatcactcg   2869

tgcattaatc gaatatgatg agagtttacg ctctgtatta cgcgcagctg gtttcgttac   2929

tcgcgatgca cgtcaagttg aacgtaaaaa agtgggttta cgcaaagcgc gtcgtcgtcc   2989

acaattctca aaacgttaat ttttctttta cgttttatat tcagattgca agcccaaaag   3049

gcttgcaatt tttttatctc aataaaattt acgataatct ttggaaatca gtgggcgatt   3109

tgtggtagaa taaacgccca ttttttatat aaaatcatgc cagaatcagg caaagtttaa   3169

taaattttaa ttcattttag agctgtcgga ggaatagatg acaagcgctg caaataaacg   3229

ttcaataatg acactttttt cagataaaac agatatttat tgccaccaag taaggattgt   3289

tttggctgaa aagggtgttg cttatgaaac ggaagttgta gatcctcaag tcgtatcaga   3349

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agatttaatg gaattaaatc cgtatggcac gttgccgaca ttagttgatc gtgatttagt 3409

gttatttaat tcacgtatta ttatggaata tcttgatgag cgtttccctc atccaccttt 3469

gatgcctgtt tatccagtgg cacgtgggaa aagccgttta ttaatgttac gtattgagca 3529

agattggtac ccagtattag caaaagctga aaaaggcacg gacgcagaac gtgctgtcgc 3589

attaaaacaa ttaagagaag agattttagc gattgcgcct attttcacgc agatgcctta 3649

ttttatgagc gaagagttta gtttagtaga ttgttatatc gccccattat tatggcgtat 3709

gcaagaactg ggtgtggatt tcagtggggc gggtagcaaa gcaattaaag cttacatggc 3769

acgtgttttt gaacgcgatt catttatgca atctttaggc gtgtcggctc cgaaaaactt 3829

aatggatgag aaataatcag tatgctacat aaatcatcac caaagcgtcc ttacttgtta 3889

agagcgtatt atgattggtt agtggataat gatttcaccc cttatttagt ggtggacgcg 3949

acttatgttg gtgtgaaagt ccctgtggaa tatgtcaaag atgggcaaat tgtcctcaat 4009

ttatctgcga atgcgacagg taatctggta ctaagcaatg aaagtattca gtttagcgcg 4069

cgttttcgtg gtatttcaca agatattttt attcctatgg gggctgcgtt agccatttat 4129

gctcgtgaaa atggtgatgg tgtactgttt gaacctgaag cgatttatga tgagctcgca 4189

acacaaaata ttggtattga gcagccactg agctttgttg aggctgtcga taaaccaaaa 4249

accagtgaga atactcaaaa aagcacaaac aaagacaaaa cgacggaaaa aaaagcgact 4309

tctcatttaa gaattattaa ataaaagagg ttttctttct tcataaaaaa acacgctttt 4369

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gctgtcatca ccaatataag ccgttcttg cgcacagaca ttggcttgtt gtatcaattc 4669

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Asp Glu Leu Leu Pro Ile Ile Val Asn Ala Asp Glu Asp Asn Lys Leu
      35   40   45

Pro Gly Arg Ser Val Leu Lys Gln Lys Asn Ile Asp Gln Gln Gln Ala
  50   55   60

Asp Asn Ala Ala Asp Leu Ile Asn Ile Leu Pro Gly Val Asn Met Ala
65   70   75   80

Gly Gly Phe Arg Pro Gly Gly Gln Thr Leu Asn Ile Asn Gly Met Gly
        85   90   95

Asp Ala Glu Asp Val Arg Val Gln Leu Asp Gly Ala Thr Lys Ser Phe
      100   105   110

Glu Lys Tyr Gln Gln Gly Ser Ile Phe Ile Glu Pro Glu Leu Leu Arg
      115   120   125

Lys Val Thr Val Asp Lys Gly Asn Tyr Ser Pro Gln Tyr Gly Asn Gly
    130   135   140

Gly Phe Ala Gly Thr Val Lys Phe Glu Thr Lys Asp Ala Thr Asp Phe
145   150   155   160

Leu Lys Glu Asn Gln Lys Ile Gly Gly Leu Phe Lys Tyr Gly Asn Asn
        165   170   175

Ser Asn Asn Asn Gln Lys Thr Tyr Ser Thr Ala Leu Val Leu Gln Asn
        180   185   190

Glu Gln Lys Asn Ile Asp Leu Leu Leu Phe Gly Ser Val Arg Asn Ala
        195   200   205

Ser Asn Tyr Thr Arg Pro Asp Lys Ser Lys Ile Leu Phe Ser Lys Asn
    210   215   220

Asn Gln Lys Ser Gly Leu Ile Lys Val Asn Trp Gln Ile Thr Pro Glu
225   230   235   240

His Leu Leu Thr Leu Ser Ser Val Tyr Gly Ile His Lys Gly Trp Glu
        245   250   255

Pro Trp Ala Ala Lys Arg Asp Val Met Ser Arg Pro Thr Glu Thr Glu
        260   265   270

Ile Lys His Tyr Gly Ile Asp Val Ala Trp Lys Arg Lys Leu Val Tyr
        275   280   285

Arg Asp Gln Lys Asp Glu Ser Tyr Ser Leu Lys Tyr Arg Tyr Leu Pro
    290   295   300

Glu Asn Asn Lys Trp Ile Asn Leu Ser Val Gln Leu Ser Tyr Ser Lys
305   310   315   320

Thr Glu Gln Asn Asp Thr Arg His Glu Lys Val Thr Ser Ser Phe Leu
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Gly Thr Leu Gly Asn Lys Ser Trp Ile Thr Tyr Ser Asp Leu Thr Phe
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Asp Ile Ser Asn Thr Ser Thr Leu Asn Ile Gly Arg Ala Glu His Glu
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Leu Leu Phe Gly Leu Gln Trp Leu Lys Asn Lys Arg Asn Thr Leu Met
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Tyr His Lys Gly Gly Val Lys Lys Ala Asp Tyr Asn Tyr Gly Tyr Phe
385                 390                 395                 400

Gln Pro Tyr Tyr Met Pro Ser Gly Arg Gln Tyr Thr Gln Ala Phe Tyr
            405                 410                 415

Leu Gln Asp Gln Ile Lys Trp Gln Asn Phe Leu Phe Thr Gly Gly Ile
            420                 425                 430

Arg Tyr Asp His Ile Asn Asn Ile Gly Gln Lys Asn Leu Ala Pro Arg
            435                 440                 445

Tyr Asn Asp Ile Ser Ala Gly His Asp Tyr Ser Gln Lys Asn Tyr Asn
    450                 455                 460

Gly Trp Ser Tyr Tyr Leu Gly Leu Lys Tyr Asp Val Asn His Tyr Leu
465                 470                 475                 480

Ser Leu Phe Thr Asn Phe Ser Lys Thr Trp Arg Ala Pro Val Ile Asp
            485                 490                 495

Glu Gln Tyr Glu Thr Gln Tyr Ser Gln Ala Ser Val Ser Ala Thr Ser
            500                 505                 510

Leu Asn Leu Glu Lys Glu Met Ile Asn Gln Thr Arg Val Gly Gly Ile
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Ile Thr Leu Asn His Leu Phe Gln Glu Asn Asp Ala Phe Gln Phe Arg
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Thr Thr Tyr Phe Tyr Asn Arg Gly Lys Asn Glu Ile Phe Lys Thr Arg
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Gly Val Asn Arg


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cctttaaata agaggctttc ttattccaac ctgtttgccc catatcactt aaactatcac 720

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71

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              Met Arg Thr Thr Thr Ile Lys Phe Ser Ala
              1                 5                 10

att aca ttg gca tta ttg agt tat tgt ggg acc att ttg gcg gat agt   4839
Ile Thr Leu Ala Leu Leu Ser Tyr Cys Gly Thr Ile Leu Ala Asp Ser
            15                20                25

cat caa gag gcg act gaa ctt gat acg att acc gtt tct tct caa caa   4887
His Gln Glu Ala Thr Glu Leu Asp Thr Ile Thr Val Ser Ser Gln Gln
            30                35                40

gat gag atg aat att aaa gag aaa aaa atc ggt gaa act gtg aaa acg   4935
Asp Glu Met Asn Ile Lys Glu Lys Lys Ile Gly Glu Thr Val Lys Thr
            45                50                55

gcg agt caa ttg aaa cgc cag caa gta cag gat agt cgt gat ctt gtg   4983
Ala Ser Gln Leu Lys Arg Gln Gln Val Gln Asp Ser Arg Asp Leu Val
        60                65                70

cgc tat gaa acc ggt gtg act gtg gta gaa gct gga cgt ttt ggt tcg   5031
Arg Tyr Glu Thr Gly Val Thr Val Val Glu Ala Gly Arg Phe Gly Ser
75                80                85                90

agc ggt tat gcc att cgt ggt gtg gat gag aac cga gta gca att aca   5079
Ser Gly Tyr Ala Ile Arg Gly Val Asp Glu Asn Arg Val Ala Ile Thr
                95                100               105

gta gat ggc tta cat caa gca gaa acc ctt tct tct caa ggc ttt aaa   5127
Val Asp Gly Leu His Gln Ala Glu Thr Leu Ser Ser Gln Gly Phe Lys
            110               115               120
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73

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gaa tta ttc gaa ggt tac ggc aat ttt aac aat acc cga aat agt gtg      5175
Glu Leu Phe Glu Gly Tyr Gly Asn Phe Asn Asn Thr Arg Asn Ser Val
        125                 130                 135

gaa att gag acg ttg aaa gtc gct aaa atc gcg aaa ggt gct gat tct      5223
Glu Ile Glu Thr Leu Lys Val Ala Lys Ile Ala Lys Gly Ala Asp Ser
        140                 145                 150

gta aaa gtg ggt agt ggt tct ttg gga ggc gct gta ctt ttt gaa aca      5271
Val Lys Val Gly Ser Gly Ser Leu Gly Gly Ala Val Leu Phe Glu Thr
155                 160                 165                 170

aaa gat gcc aga gat ttc ctg act gaa aaa gat tgg cat atc ggc tat      5319
Lys Asp Ala Arg Asp Phe Leu Thr Glu Lys Asp Trp His Ile Gly Tyr
                175                 180                 185

aaa gcg ggc tac tca acg gca gat aat cag gga tta aat gca gtg act      5367
Lys Ala Gly Tyr Ser Thr Ala Asp Asn Gln Gly Leu Asn Ala Val Thr
                190                 195                 200

ctt gca ggt cgc tat caa atg ttt gat gca ttg att atg cat tct aag      5415
Leu Ala Gly Arg Tyr Gln Met Phe Asp Ala Leu Ile Met His Ser Lys
                205                 210                 215

cga cat gga cat gaa tta gaa aat tat gac tat aaa aat ggc aga gat      5463
Arg His Gly His Glu Leu Glu Asn Tyr Asp Tyr Lys Asn Gly Arg Asp
        220                 225                 230

att caa ggg aaa gaa aga gag aaa gcg gat cct tat acg att acg aaa      5511
Ile Gln Gly Lys Glu Arg Glu Lys Ala Asp Pro Tyr Thr Ile Thr Lys
235                 240                 245                 250

gaa agt aca tta gtg aaa ttc tct ttt tcg cca aca gaa aat cat cgt      5559
Glu Ser Thr Leu Val Lys Phe Ser Phe Ser Pro Thr Glu Asn His Arg
                255                 260                 265

ttt aca gtc gct tct gat act tat ctt cag cat tcc cgc gga cat gat      5607
Phe Thr Val Ala Ser Asp Thr Tyr Leu Gln His Ser Arg Gly His Asp
                270                 275                 280

ctt tca tat aat ctt gtt gca aca aca cat att cag tta gat gag aaa      5655
Leu Ser Tyr Asn Leu Val Ala Thr Thr His Ile Gln Leu Asp Glu Lys
                285                 290                 295

gaa tct cgt cat gca aat gat ttg aca aaa cgt aaa aat gtt tcc ttt      5703
Glu Ser Arg His Ala Asn Asp Leu Thr Lys Arg Lys Asn Val Ser Phe
        300                 305                 310

act tat gaa aat tat act gtt acg cca ttt tgg gat acg ctc aag tta      5751
Thr Tyr Glu Asn Tyr Thr Val Thr Pro Phe Trp Asp Thr Leu Lys Leu
315                 320                 325                 330

agc tat tca caa caa aga att aca aca aga gca aga aca gaa gat tat      5799
Ser Tyr Ser Gln Gln Arg Ile Thr Thr Arg Ala Arg Thr Glu Asp Tyr
                335                 340                 345

tgt gat gga aat gag tta tgt gat tct tat aaa aat cca tta ggt ctc      5847
Cys Asp Gly Asn Glu Leu Cys Asp Ser Tyr Lys Asn Pro Leu Gly Leu
                350                 355                 360

caa ttt aaa gat ggt cag att ctt gat cct gca ggg aat aaa att aaa      5895
Gln Phe Lys Asp Gly Gln Ile Leu Asp Pro Ala Gly Asn Lys Ile Lys
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74

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       cta cag ggg tct gga ttg agc act cag att gta gat gaa aat gga aaa   5943
       Leu Gln Gly Ser Gly Leu Ser Thr Gln Ile Val Asp Glu Asn Gly Lys
           380             385             390

       cca ttt cct aca aca aca ggt act aat aat gct gct ttt agt aat aat   5991
       Pro Phe Pro Thr Thr Thr Gly Thr Asn Asn Ala Ala Phe Ser Asn Asn
       395             400             405             410

       tta cga ctc agg cct aca ggt ttt tgg tta gat tgc tcg gtt ttt gac   6039
       Leu Arg Leu Arg Pro Thr Gly Phe Trp Leu Asp Cys Ser Val Phe Asp
                   415             420             425

       tgt aat aaa cca ttc act gtt tat aat att agt aat gga aca tat caa   6087
       Cys Asn Lys Pro Phe Thr Val Tyr Asn Ile Ser Asn Gly Thr Tyr Gln
                   430             435             440

       gca aga gag gtt cta ctg tct gaa gag ata act gtg gat ggt aaa tta   6135
       Ala Arg Glu Val Leu Leu Ser Glu Glu Ile Thr Val Asp Gly Lys Leu
               445             450             455

       tac aaa aca gct aag gaa gaa gga ggg ctt cca aat tat ttg att tta   6183
       Tyr Lys Thr Ala Lys Glu Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu
           460             465             470

       cct aat tct aaa ggt tat ctt cct tat gat tat aaa gaa agg gat ctt   6231
       Pro Asn Ser Lys Gly Tyr Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu
       475             480             485             490

       aat acg aat aca aaa caa att aat tta gat tta act aaa aca ttt tta   6279
       Asn Thr Asn Thr Lys Gln Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu
                   495             500             505

       act ttc aac atc gaa aat aat ctg tca tat ggt gga gtt tat tct cgg   6327
       Thr Phe Asn Ile Glu Asn Asn Leu Ser Tyr Gly Gly Val Tyr Ser Arg
                   510             515             520

       ata gag aaa gaa atg att aat aaa gct ggt tat gag ggg aga aat cct   6375
       Ile Glu Lys Glu Met Ile Asn Lys Ala Gly Tyr Glu Gly Arg Asn Pro
                   525             530             535

       act tgg tgg gct gat aga att tta ggg caa agt agt tac tgt ggt tat   6423
       Thr Trp Trp Ala Asp Arg Ile Leu Gly Gln Ser Ser Tyr Cys Gly Tyr
           540             545             550

       aat gca ttg aag tgt ccg aaa cat gag cca tta acg tca ttt tta att   6471
       Asn Ala Leu Lys Cys Pro Lys His Glu Pro Leu Thr Ser Phe Leu Ile
       555             560             565             570

       cca gtt gaa gca acg aca cag tca tta tat ttt gca aat att ctt aag   6519
       Pro Val Glu Ala Thr Thr Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys
                   575             580             585

       gta cat aat atg att agc ata gat tta gga tat cgt tat gat cat att   6567
       Val His Asn Met Ile Ser Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile
                   590             595             600

       aaa tat aac cct gaa tac act cca gga gta act cca aaa att cca gat   6615
       Lys Tyr Asn Pro Glu Tyr Thr Pro Gly Val Thr Pro Lys Ile Pro Asp
                   605             610             615
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75

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gat atg gta aaa ggt ttg ttt att cct atg cca aaa gag cca cag cta    6663
Asp Met Val Lys Gly Leu Phe Ile Pro Met Pro Lys Glu Pro Gln Leu
    620             625             630

aag gat ttt gat tat aac tat gct aaa ttt ggt gag gcc tat aaa aaa    6711
Lys Asp Phe Asp Tyr Asn Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys
635             640             645             650

tgg aaa gaa tat ctg cca aaa aat gcg gaa gaa aat att gct tac att    6759
Trp Lys Glu Tyr Leu Pro Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile
                655             660             665

gct caa gat aag aca ttt aaa aaa cat tct tat tct ctt ggt gca act    6807
Ala Gln Asp Lys Thr Phe Lys Lys His Ser Tyr Ser Leu Gly Ala Thr
            670             675             680

ttc gat cct ctg aat ttt tta cga gta caa gta aaa tat tca aaa ggg    6855
Phe Asp Pro Leu Asn Phe Leu Arg Val Gln Val Lys Tyr Ser Lys Gly
            685             690             695

ttt aga gcc ccg act tcg gat gaa ctt tat ttt acc ttt aag cat cca    6903
Phe Arg Ala Pro Thr Ser Asp Glu Leu Tyr Phe Thr Phe Lys His Pro
    700             705             710

gat ttt acg att tta ccg aac ccc gtg ttg aaa cca gag gaa gca aaa    6951
Asp Phe Thr Ile Leu Pro Asn Pro Val Leu Lys Pro Glu Glu Ala Lys
715             720             725             730

aat caa gag att gca tta aca gtg cac gat aat tgg gga ttt gtt agc    6999
Asn Gln Glu Ile Ala Leu Thr Val His Asp Asn Trp Gly Phe Val Ser
                735             740             745

aca agt gtt ttc caa aca aag tat cgt cat ttt att gat tta gcg tat    7047
Thr Ser Val Phe Gln Thr Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr
            750             755             760

tta ggt tca aga aat tta tcg aat tcc gtg gga ggg cag gca caa gca    7095
Leu Gly Ser Arg Asn Leu Ser Asn Ser Val Gly Gly Gln Ala Gln Ala
            765             770             775

aga gat ttc caa gtt tat caa aat gtc aat gtc gat aat gcc aaa gtt    7143
Arg Asp Phe Gln Val Tyr Gln Asn Val Asn Val Asp Asn Ala Lys Val
            780             785             790

aaa gga ctt gaa att aat gca cgt ttg aat ttg gga tat ttt tgg cat    7191
Lys Gly Leu Glu Ile Asn Ala Arg Leu Asn Leu Gly Tyr Phe Trp His
795             800             805             810

gtg ttg gat gga ttt aat acg agc tat aaa ttc act tac caa cgt ggt    7239
Val Leu Asp Gly Phe Asn Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly
                815             820             825

cgt ttg gat ggc gat cgt cca atg aat gcg att cag cct aaa gct tct    7287
Arg Leu Asp Gly Asp Arg Pro Met Asn Ala Ile Gln Pro Lys Ala Ser
            830             835             840

gtt ttt ggt ttg ggc tac gat cat aaa gaa aat aaa ttt ggc gct gat    7335
Val Phe Gly Leu Gly Tyr Asp His Lys Glu Asn Lys Phe Gly Ala Asp
            845             850             855

tta tat att aca cgt gtg agt gag aaa aaa gcg aaa gac act tat aat    7383
Leu Tyr Ile Thr Arg Val Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn
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76

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atg ttc tat aaa gaa cag gga tat aaa gat agt gct gtt cgt tgg aga    7431
Met Phe Tyr Lys Glu Gln Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg
875             880             885             890

agt gat gac tat acg cta gtt gat gcg gtt ggt tat att aaa ccg att    7479
Ser Asp Asp Tyr Thr Leu Val Asp Ala Val Gly Tyr Ile Lys Pro Ile
                895             900             905

aag aat tta acg tta cag ttt ggc gtt tat aat ttg aca gac cgt aaa    7527
Lys Asn Leu Thr Leu Gln Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys
                910             915             920

tac ttg aca tgg gaa tct gct cgt tcg att aaa cca ttt ggt aca agt    7575
Tyr Leu Thr Trp Glu Ser Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser
                925             930             935

aat tta att aat caa aaa aca ggc gca gga att aat cgt ttt tac tca    7623
Asn Leu Ile Asn Gln Lys Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser
                940             945             950

cca ggt cgt aac ttt aaa ctc agt gcc gaa atc acc ttc taatcctaag    7672
Pro Gly Arg Asn Phe Lys Leu Ser Ala Glu Ile Thr Phe
955             960             965

cctgcgtatg caggctttct ttttagggaa agtgcggtgg atttgacaaa gatttattgc    7732

ttttctgtaa atcaatgcta aaattcacac tcctttgtcg tagctggatt agagatcggc    7792

tagcgatgta tttttaactt aacttttagg agttatcaaa tgtctctaag tacagaaaaa    7852

aaagcagcaa ttgttgctga atttggtcgt gatgcaaaag ataccggttc ttcagaagtg    7912

caaatcgcat tattaactgc acaaatcaac cacttacaat ctcactttgc aacgcacaaa    7972

aaagaccacc acggtcgtcg tggtttattg cgtatggttt ctcgtcgtcg taaactttta    8032

gattacttaa aacgtactaa tcttgagctt tacacttcaa ctatcgctcg tttaggttta    8092

cgtcgctaat ttgtattagg atttattcca aacaaaaaac ccttgataat tttatcaagg    8152

gttttctttt ttctgcatac taggcatgtt taaattatcg caaaacacac cgcacatttc    8212

gtggaaaagt gcggtcattt tttaatttta ttttacttct ttaaacatga tctcacttgg    8272

gattactgaa ccttgccagt aaagctcagt agcgactttt tcagctaatt gcataaacga    8332

ttgggcaatg tcgctttcag gtgcggcgac aacggttggg atacctttgt ctaaatcttc    8392

acgtaagcga atatgtaatg cctgttgtcc taaaactttg acattatatt tttgtgcaat    8452

gcgctcagca ccgcctgttc cgaaaatcgt ttcttgatga ccacaattgc tacaaatatg    8512

catcgacata ttttcgataa tgcctaaaac gggtacagaa acacgctcaa acatcgccac    8572

acctttaatc gcatccagta aagcaatatc ttgtggtgtt gtcaccacga ccgcccccgt    8632

cactggaatt tgttgagaaa gggtcagctg gatatcccct gtacccggtg gcatatcaat    8692

gactaaataa tctaaatcag gccataaggt ttcttgcaaa agctgactta aggcactgct    8752
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77

```
tgccattgga ccgcgccaaa tcgtagcatt gtccggttcc attaagaaac caatggaatt 8812

ggcaaaaata tgatgtgctt gaattggggt aatgtgctgg ttatctggcg aagttgggcg 8872

ttgatcagca acccctaaca tgtgtggaat agatggacca taaatatcgg catctaaaat 8932

tccaacacga gcaccttgtc tttgtaaggc aagagcaaga ttgacggaaa tagtagattt 8992

tcctacacca cctttacccg atgtcacggc aataatattt tttacccctt ttacggctgg 9052

gtggctatta gcgcgtttta atgtcgcgat ttgataattt aattgccatt tgatgtcttt 9112

gcattctgct aatgtgagaa gttctgtgga gagagcgctc ttgagttgtt cgaatgcagt 9172

attccaagca aacggcatgc tgatttcaat acgtaacgtc tcaccgcctt tttcaatttt 9232

tttgatagca tttaggctga cgagatcttt ttgtaagcta ggatgttgaa attgttgaaa 9292

tgtgttttgg atagcttgtt tttgactgtc cgttaaactg tcagaaaata aaattcccat 9352

tgattttatc ccgttatttt tggtggctaa ttaaagccct agttaatcac tcaactatat 9412

ttaaccacga agctgtagaa ctgttaagca gaaatgtgga aaagcgcggt taaagtagaa 9472

aaaatactgc gaataaggta acataagcgc caattttttg atgaaaaata ggaatgataa 9532

catggcaaat tcggcacgcg atattttggt cacttgcgcc ttaccttatg caaatggtgc 9592

aattcattta gggcatttat tagaacatat tcaagcagat atttgggtgc gttccaacgt 9652

atgcgtgggc ataaagtgca tttttatttgt gcagatgatg cccatggcac accaatcatg 9712

ttaaatgcga taaattaggt attacaccaa agcattaatt gctcctcgaa agcagaacat 9772

gtggcggatt tgaaggctta atattagcta tgataatatc at            9814
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<210> 32
<211> 967
<212> PRT
<213> Pasteurella multocida

<400> 32
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Met Arg Thr Thr Thr Ile Lys Phe Ser Ala Ile Thr Leu Ala Leu Leu
 1               5                   10                  15

Ser Tyr Cys Gly Thr Ile Leu Ala Asp Ser His Gln Glu Ala Thr Glu
            20                  25                  30

Leu Asp Thr Ile Thr Val Ser Ser Gln Gln Asp Glu Met Asn Ile Lys
        35                  40                  45

Glu Lys Lys Ile Gly Glu Thr Val Lys Thr Ala Ser Gln Leu Lys Arg
    50                  55                  60

Gln Gln Val Gln Asp Ser Arg Asp Leu Val Arg Tyr Glu Thr Gly Val
65                  70                  75                  80

Thr Val Val Glu Ala Gly Arg Phe Gly Ser Ser Gly Tyr Ala Ile Arg
                85                  90                  95

Gly Val Asp Glu Asn Arg Val Ala Ile Thr Val Asp Gly Leu His Gln
```

78

```
            100                    105                    110

Ala Glu Thr Leu Ser Ser Gln Gly Phe Lys Glu Leu Phe Glu Gly Tyr
        115                120                125

Gly Asn Phe Asn Asn Thr Arg Asn Ser Val Glu Ile Glu Thr Leu Lys
        130                135                140

Val Ala Lys Ile Ala Lys Gly Ala Asp Ser Val Lys Val Gly Ser Gly
145                150                155                160

Ser Leu Gly Gly Ala Val Leu Phe Glu Thr Lys Asp Ala Arg Asp Phe
                165                170                175

Leu Thr Glu Lys Asp Trp His Ile Gly Tyr Lys Ala Gly Tyr Ser Thr
            180                185                190

Ala Asp Asn Gln Gly Leu Asn Ala Val Thr Leu Ala Gly Arg Tyr Gln
        195                200                205

Met Phe Asp Ala Leu Ile Met His Ser Lys Arg His Gly His Glu Leu
        210                215                220

Glu Asn Tyr Asp Tyr Lys Asn Gly Arg Asp Ile Gln Gly Lys Glu Arg
225                230                235                240

Glu Lys Ala Asp Pro Tyr Thr Ile Thr Lys Glu Ser Thr Leu Val Lys
                245                250                255

Phe Ser Phe Ser Pro Thr Glu Asn His Arg Phe Thr Val Ala Ser Asp
                260                265                270

Thr Tyr Leu Gln His Ser Arg Gly His Asp Leu Ser Tyr Asn Leu Val
            275                280                285

Ala Thr Thr His Ile Gln Leu Asp Glu Lys Glu Ser Arg His Ala Asn
        290                295                300

Asp Leu Thr Lys Arg Lys Asn Val Ser Phe Thr Tyr Glu Asn Tyr Thr
305                310                315                320

Val Thr Pro Phe Trp Asp Thr Leu Lys Leu Ser Tyr Ser Gln Gln Arg
                325                330                335

Ile Thr Thr Arg Ala Arg Thr Glu Asp Tyr Cys Asp Gly Asn Glu Leu
            340                345                350

Cys Asp Ser Tyr Lys Asn Pro Leu Gly Leu Gln Phe Lys Asp Gly Gln
        355                360                365

Ile Leu Asp Pro Ala Gly Asn Lys Ile Lys Leu Gln Gly Ser Gly Leu
        370                375                380

Ser Thr Gln Ile Val Asp Glu Asn Gly Lys Pro Phe Pro Thr Thr Thr
385                390                395                400

Gly Thr Asn Asn Ala Ala Phe Ser Asn Asn Leu Arg Leu Arg Pro Thr
                405                410                415

Gly Phe Trp Leu Asp Cys Ser Val Phe Asp Cys Asn Lys Pro Phe Thr
                420                425                430
```

79

Val Tyr Asn Ile Ser Asn Gly Thr Tyr Gln Ala Arg Glu Val Leu Leu
    435   440   445

Ser Glu Glu Ile Thr Val Asp Gly Lys Leu Tyr Lys Thr Ala Lys Glu
    450   455   460

Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu Pro Asn Ser Lys Gly Tyr
465   470   475   480

Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu Asn Thr Asn Thr Lys Gln
            485   490   495

Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu Thr Phe Asn Ile Glu Asn
            500   505   510

Asn Leu Ser Tyr Gly Gly Val Tyr Ser Arg Ile Glu Lys Glu Met Ile
    515   520   525

Asn Lys Ala Gly Tyr Glu Gly Arg Asn Pro Thr Trp Trp Ala Asp Arg
    530   535   540

Ile Leu Gly Gln Ser Ser Tyr Cys Gly Tyr Asn Ala Leu Lys Cys Pro
545   550   555   560

Lys His Glu Pro Leu Thr Ser Phe Leu Ile Pro Val Glu Ala Thr Thr
            565   570   575

Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys Val His Asn Met Ile Ser
            580   585   590

Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile Lys Tyr Asn Pro Glu Tyr
            595   600   605

Thr Pro Gly Val Thr Pro Lys Ile Pro Asp Asp Met Val Lys Gly Leu
    610   615   620

Phe Ile Pro Met Pro Lys Glu Pro Gln Leu Lys Asp Phe Asp Tyr Asn
625   630   635   640

Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys Trp Lys Glu Tyr Leu Pro
            645   650   655

Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile Ala Gln Asp Lys Thr Phe
            660   665   670

Lys Lys His Ser Tyr Ser Leu Gly Ala Thr Phe Asp Pro Leu Asn Phe
            675   680   685

Leu Arg Val Gln Val Lys Tyr Ser Lys Gly Phe Arg Ala Pro Thr Ser
    690   695   700

Asp Glu Leu Tyr Phe Thr Phe Lys His Pro Asp Phe Thr Ile Leu Pro
705   710   715   720

Asn Pro Val Leu Lys Pro Glu Glu Ala Lys Asn Gln Glu Ile Ala Leu
            725   730   735

Thr Val His Asp Asn Trp Gly Phe Val Ser Thr Ser Val Phe Gln Thr
            740   745   750

Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr Leu Gly Ser Arg Asn Leu
    755   760   765

80

```
Ser Asn Ser Val Gly Gly Gln Ala Gln Ala Arg Asp Phe Gln Val Tyr
    770             775             780
```
```
Gln Asn Val Asn Val Asp Asn Ala Lys Val Lys Gly Leu Glu Ile Asn
785             790             795             800
```
```
Ala Arg Leu Asn Leu Gly Tyr Phe Trp His Val Leu Asp Gly Phe Asn
            805             810             815
```
```
Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly Arg Leu Asp Gly Asp Arg
            820             825             830
```
```
Pro Met Asn Ala Ile Gln Pro Lys Ala Ser Val Phe Gly Leu Gly Tyr
        835             840             845
```
```
Asp His Lys Glu Asn Lys Phe Gly Ala Asp Leu Tyr Ile Thr Arg Val
    850             855             860
```
```
Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn Met Phe Tyr Lys Glu Gln
865             870             875             880
```
```
Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg Ser Asp Asp Tyr Thr Leu
            885             890             895
```
```
Val Asp Ala Val Gly Tyr Ile Lys Pro Ile Lys Asn Leu Thr Leu Gln
        900             905             910
```
```
Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys Tyr Leu Thr Trp Glu Ser
        915             920             925
```
```
Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser Asn Leu Ile Asn Gln Lys
    930             935             940
```
```
Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser Pro Gly Arg Asn Phe Lys
945             950             955             960
```
```
Leu Ser Ala Glu Ile Thr Phe
                965
```

<210> 33
<211> 2990
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1106)..(1564)

<220>
<223> kdtB

<400> 33
gtcaacccct ttggctttga gttgtgctaa taaagcatcg tcaaaatgca agccggcagt 60

tggtgccgca accgcgccag ggactttgtt ataaacggtt tgataacgtt ctttatccgc 120

ttcttcgtca gggcgatcaa tataagggggg caatggcata tgcccaattt gctgtaacac 180

gtctaaaagt gcggtctgtt tttgcgcgat ttctaattca aataaggtat catggcgcgc 240

aaccatgatc attttgacac catgatgttc acctaactta tcttcgccta accacagttc 300
```

tgccccttct ttcggtgctt ttgaggagcg cacatgggct aaaaagcgtg tgtcggataa 360

aatccgctcg accaacactt ccaccttacc gccactggct ttacgtccaa acatccttgc 420

aggaatcacg cgcgtgttat taaaaattaa taagtcgcct tcatgaattt gatcaaggat 480

atcagcaaaa gtgcggtggg taatctcacc attttcgccg ttaagttgta ataagcgact 540

agcggtgcga tccggttttg ggtaacgagc aatcagctca tcgggtaaat caaaataaaa 600

gtcagaaaca cgcataaata gggttataaa aagttatcta aaaaatcgtg ggcgtaagtc 660

tagtgtgaat tccgctcttg cacaaggaaa aatccagatt ttgttgttta gtatcgaatt 720

gagatgattt tggacaaaaa aaaagccctt tcaagaaaga cgaaagggcg aaaatatatt 780

tggagtcata ctttttaggg tatgtgtcgg attatacaca caaaaataac aaatgcaaca 840

tttttttaac aatcatatgt aagcgtattg tgtgagaacg agcgtaaaaa tgaacgcatt 900

ctaaaggatg atttatttag cctattaaaa aaacacatga gatgagagtt tgcgagagcg 960

gtaataaaag tgcggtgggt tttagaaaag ttttgaatag gatcacaaat aaacaaagt 1020

ttgtgaaata ccaagtagta gtttttaagt atatgatgaa tcatatgcta agtttaaac 1080

ccgttaaata accaagaggt ggaag atg aca gaa gaa aat aaa gga aag aga    1132
                           Met Thr Glu Glu Asn Lys Gly Lys Arg
                            1                   5

tat ttt tta tgg ttc ata ttg ttt atc ctt tca atc tat tta ttt att  1180
Tyr Phe Leu Trp Phe Ile Leu Phe Ile Leu Ser Ile Tyr Leu Phe Ile
 10              15                  20                  25

acc ata caa gaa aga cga ggt tat tgt ttt gac aaa cgt gca tat att  1228
Thr Ile Gln Glu Arg Arg Gly Tyr Cys Phe Asp Lys Arg Ala Tyr Ile
                30              35                  40

cat gag ctt tat act gag caa gag tta att gat cgg ggg att gaa tat  1276
His Glu Leu Tyr Thr Glu Gln Glu Leu Ile Asp Arg Gly Ile Glu Tyr
            45                  50                  55

gtg gta tcc acc atg ccg tca ggt gtt att aaa cca gat ggc aca ata  1324
Val Val Ser Thr Met Pro Ser Gly Val Ile Lys Pro Asp Gly Thr Ile
                60                  65                  70

aaa gaa gta aag cgt tac acg agt gtc gag gag ttt aaa cag atg aac  1372
Lys Glu Val Lys Arg Tyr Thr Ser Val Glu Glu Phe Lys Gln Met Asn
        75                  80                  85

cca gct tgt tgt aca tta acc acc ttt att gat gaa gga ggc gat ggc  1420
Pro Ala Cys Cys Thr Leu Thr Thr Phe Ile Asp Glu Gly Gly Asp Gly
 90                  95                  100                 105

tat cca gat gat gat gga tat ggt tat gtc aga att gaa tat tta aga  1468
Tyr Pro Asp Asp Asp Gly Tyr Gly Tyr Val Arg Ile Glu Tyr Leu Arg
                    110                 115                 120

cat tat gtt gag aat cta aaa cct tat cat aga gtg att tat ctt gaa  1516
His Tyr Val Glu Asn Leu Lys Pro Tyr His Arg Val Ile Tyr Leu Glu
                125                 130                 135

82

```
tat acg ccc tgt gga gag tta agg gaa gag gcg gct ttt tca aaa aat    1564
Tyr Thr Pro Cys Gly Glu Leu Arg Glu Glu Ala Ala Phe Ser Lys Asn
        140                 145                 150

taagagtgag gtgaagaaat ggcattacca acagcaacaa taatgaggaa tttatcttta 1624

tctaaaaatc aattcactct gaaagggatg gaatgcgtag attccctatt tcaagcatgc 1684

agtaatatgg atcatgggta ctgaggtgga agatggcaga agaaataaa ggaaagagat 1744

attttttatg gttcatattg tttatccttt caatctattt atttattacc atacaagaaa 1804

gacgaggtta ttgttttgac aaatgggaat atatccataa cctttatacc gagcaagagt 1864

tgatcgatag aggggttgaa tatgtggtat ccaccatgcc gtcaggtgtt tttgaaccag 1924

atggcacaac aaccgaaata aaacgttatg ctagtgttga ggagtttaaa cagatgaacc 1984

ctgattgttg taaattaaca agatttatta atgaaggaat agatggctat ccagatgatg 2044

atggatatgg ttatataaga attgaatatt taagacatta tgttgggaat tttaaacctg 2104

atcatagagt gctttatctc gaatatacgc cttgtggaga attaagggaa gaggtttctt 2164

tttaaaaaat aaataatagt gaggtgaaga aatggcatta ccaacagcaa cagaaatcac 2224

aaatgcatat ttatataaaa ataaattaac tcctaaagcg gaggaaagag tagattcaat 2284

acaaattctt gaaaaggag atgaacattt cgaagtaaat tttaattgat caaagtactc 2344

tattgattga aggaaaaaca gtggaattaa tggcaggtat ggcagtttct gcggaaatta 2404

aaacaggtaa acgcagtgta ttagattact tatttagccc attaaaaacc acaaaataat 2464

attaaggaga ataatatgtc gtataataaa tatactgttg ctttgattac gttctcaaca 2524

gggatctgta ttccggcaat atgctacgct ctaaattcgc tgggatacag atcctgtttg 2584

agactatgta gaaaagacta aactttgtgt ggttaactgg gcttcggtaa aattctggaa 2644

acaaatgggc ttaacccgcg tgatcttatc ccgtgagctt tcgcttgatg aaattgccga 2704

aattcgtcag caagtgccag aaatggaaat tgaagtgttc gtgcatgggg cattatgcat 2764

ggcgtattct ggacgttgtt tattatcagg ctatattaat aaacgtgatc caaatcaagg 2824

cacctgtacc aatgcgtgcc gttgggaata cagtgtaacc gaagccaaag aagatgagat 2884

cggcaacatt gtgaatgtgg gtgaagaaat tccagtgaaa aatgtagcac cgacacttgg 2944

cgaaggcgac accaccagta aagtattttt attagcagaa agtcga         2990


<210> 34
<211> 153
<212> PRT
<213> Pasteurella multocida

<400> 34
Met Thr Glu Glu Asn Lys Gly Lys Arg Tyr Phe Leu Trp Phe Ile Leu
  1               5                  10                  15
```

83

```
Phe Ile Leu Ser Ile Tyr Leu Phe Ile Thr Ile Gln Glu Arg Arg Gly
            20              25                  30

Tyr Cys Phe Asp Lys Arg Ala Tyr Ile His Glu Leu Tyr Thr Glu Gln
        35              40                  45

Glu Leu Ile Asp Arg Gly Ile Glu Tyr Val Val Ser Thr Met Pro Ser
    50                  55                  60

Gly Val Ile Lys Pro Asp Gly Thr Ile Lys Glu Val Lys Arg Tyr Thr
65                  70                  75                  80

Ser Val Glu Glu Phe Lys Gln Met Asn Pro Ala Cys Cys Thr Leu Thr
                85                  90                  95

Thr Phe Ile Asp Glu Gly Gly Asp Gly Tyr Pro Asp Asp Asp Gly Tyr
            100             105                 110

Gly Tyr Val Arg Ile Glu Tyr Leu Arg His Tyr Val Glu Asn Leu Lys
        115                 120                 125

Pro Tyr His Arg Val Ile Tyr Leu Glu Tyr Thr Pro Cys Gly Glu Leu
    130                 135                 140

Arg Glu Glu Ala Ala Phe Ser Lys Asn
145                 150


<210> 35
<211> 1683
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (325)..(1230)

<220>
<223> lgtC

<400> 35
atatcaaagt ctcatggcaa gaaaattaga aaagagcgat caattattat ttgcaagatt 60

tgggtattat tcataggcta ggtgaaagat atattttttcc atgatattaa aacgattcag 120

gcagaactgg ctagcttatc acttttagat aattgtatta ttaaaagaag ctgtatgatt 180

gttattctat cattagtgga taataaatat tctttatttt ttgagagata aaaacaattc 240

atatttcaat agaaaacaga aaataaagat tatcaaaaga attatccgtc cttataaata 300

tgagtctgta ttgtgagatg atat atg aat att tta ttt gtt tct gat gat    351
                         Met Asn Ile Leu Phe Val Ser Asp Asp
                          1               5

gtt tat gct aaa cat ctg gtg gtt gcg att aaa agc att ata aat cat  399
Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His
 10              15                  20                  25

aat gaa aaa ggt att tca ttt tat att ttt gat ttg ggt ata aag gat  447
Asn Glu Lys Gly Ile Ser Phe Tyr Ile Phe Asp Leu Gly Ile Lys Asp
                30                  35                  40
```

84

```
gaa aat aag aga aat att aat gat att gtt tct tct tat gga agt gaa      495
Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu
            45              50                  55

gtc aac ttt att gct gtg aat gag aaa gaa ttt gag agt ttt cct gtt      543
Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val
        60                  65                  70

caa att agt tat att tct tta gca aca tat gca agg cta aaa gcg gca      591
Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala
        75                  80                  85

gag tat ttg ccg gat aat tta aat aaa att att tat tta gat gtt gat      639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp
90                  95                  100                 105

gtt ttg gtt ttt aac tca tta gaa atg tta tgg aat gtt gat gtt aat      687
Val Leu Val Phe Asn Ser Leu Glu Met Leu Trp Asn Val Asp Val Asn
                110                 115                 120

aat ttt ctt acc gca gcc tgt tat gat tct ttc atc gaa aat gaa aag      735
Asn Phe Leu Thr Ala Ala Cys Tyr Asp Ser Phe Ile Glu Asn Glu Lys
                125                 130                 135

tct gag cat aaa aaa tcg att tca atg tca gat aag gaa tat tat ttt      783
Ser Glu His Lys Lys Ser Ile Ser Met Ser Asp Lys Glu Tyr Tyr Phe
            140                 145                 150

aat gca gga gta atg cta ttt aat tta gat gaa tgg cgg aag atg gat      831
Asn Ala Gly Val Met Leu Phe Asn Leu Asp Glu Trp Arg Lys Met Asp
        155                 160                 165

gta ttc tca aga gct tta gac ctg tta gct atg tat cct aat caa atg      879
Val Phe Ser Arg Ala Leu Asp Leu Leu Ala Met Tyr Pro Asn Gln Met
170                 175                 180                 185

att tat cag gat caa gat ata ttg aat atc ctt ttt agg aat aaa gtc      927
Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val
                190                 195                 200

tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga      975
Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg
                205                 210                 215

ata aan caa tac cat aaa gga aaa ntg agc aac tta cat tct tta gaa      1023
Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu
            220                 225                 230

aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa      1071
Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys
            235                 240                 245

gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa      1119
Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys
250                 255                 260                 265

ata tta gca naa atn tcg aga ggc ncg gat aaa gaa cgc gta tta tct      1167
Ile Leu Ala Xaa Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser
            270                 275                 280

ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc      1215
Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe
```

85

aaa tat caa gtc tat taactattga atttttgcaa atgagataag agtatagtgc   1270
Lys Tyr Gln Val Tyr
            300

tgatttcttc aaagcgaaaa ggaggaaata gcttgttcta atttattaca ataatggttg 1330

tattcatctt gattttgaag gaaagagagt gttttttgta taaaagcatt ttcgtcacct 1390

aaatttacta atcctccaaa ttctcctcct cgnagaattt ctttcggacc ggtagggcag 1450

tccatggata ttacaggtgt accgcaagcc atgctttcta ggataactgt cggtaacccc 1510

tctttcaaag aggtgtgtaa aaatagctta gcattttta ttaatggata cggattatct 1570

ttatttccta aaagaaaaca atcttcttgt agattgagtg attctatttg tttctctaat 1630

ttttctcgac actcaccatc ccaaacaata tatancnttt cttggatacc tcc   1683

<210> 36
<211> 302
<212> PRT
<213> Pasteurella multocida

<400> 36
Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
 1   5   10   15

Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
            20   25   30

Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
            35   40   45

Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
        50   55   60

Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65   70   75   80

Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
                85   90   95

Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
                100   105   110

Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
            115   120   125

Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
        130   135   140

Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
145   150   155   160

Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
                165   170   175

Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
            180   185   190

86

```
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
        195             200             205
```

```
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly
    210             215             220
```

```
Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
225             230             235             240
```

```
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
            245             250             255
```

```
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg
            260             265             270
```

```
Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
    275             280             285
```

```
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
    290             295             300
```

<210> 37
<211> 2029
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (2)..(499)

<220>
<223> mglB

<400> 37
```
c tta aat aaa gcc ggt aaa att caa tac gtt tta tta aaa ggt aac caa   49
  Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln
    1           5               10              15
```

```
gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta   97
Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
            20              25              30
```

```
nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg   145
Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
            35              40              45
```

```
tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc   193
Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
    50              55              60
```

```
tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg   241
Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
65              70              75              80
```

```
gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca   289
Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
                85              90              95
```

```
atc ttc ngt gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa   337
Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
            100             105             110
```

87

```
ggt gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa    385
Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
        115             120             125

gcc gtt gtt caa tta agt aat aat ctt gca aaa gga aaa cct gcc act    433
Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
        130             135             140

gaa ggc aca aaa tgg cag tta aaa cga tcg tgt cct acg tat ccc tta    481
Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
145             150             155             160

tgt tgg tgt gga tgc gga  taacttaaac gagttcctaa aataataaac         529
Cys Trp Cys Gly Cys Gly
                165

tataacaaaa caagamgttg taattctcgg ggaggtatac cctcccccctt tttatgtgag 589

gttggatatg acaactcaaa ttccaaatca agacagtgaa atactgctca caatgaccaa 649

cgtctgtaaa tcctttcccg gtgttaaagc gttagacaat gcaaacctaa ctgtgcgctc 709

gcattctgtc catgccttaa tgggcgaaaa tggggcgggc aaatcgacct tattaaaatg 769

cttatttggt atttacagta aagatgaagg tgacatcctt ttcttaggca agccagtcaa 829

ctttaaaacg tcgaaagaag ccttagagaa cgggattttc atggtgcacc aagaacttaa 889

cttggttaaa caatgtactg taatggataa tcctttggnt aggacgttat ccattaaaag 949

caggctttgt cgatcacggc aaaatgtatc gtgataccaa agcagatttt tgaagaanta 1009

gatatcgata tcgatccaaa agaaaaagtg gccaaattgt cagtgtcaca aatgcaaatg 1069

atcgagatcg caaaggcctt ttcatacaat gccaaaatcg taatcatgga cgaaccgact 1129

tcttcgcttt cagaaaaaga agttgaacac ctatttaaaa ttatcgcgaa gctaaaacaa 1189

cgtggctgtg cattattta tatttcgcac aaaatggacg aaatcttcaa aatttgtgac 1249

gaaattacga ttttacgcga tggtaaatgg atcaatacgg tcgctgttaa aggcaccaca 1309

atggatcaga ttgtatccat gatggttggg cgtgaactca cgcaacgttt cccaccaaaa 1369

accaataccc caaaagaaac catcttaacg gtggaaaatc tgaccgcact taatcagcca 1429

tctattcaag atgttagttt tgaattacgc aaaggcgaag tgctcggcat tgcgggactg 1489

gttggggcaa aacggtaccg atattgtgga aacgatcttc ggggtgcgtg aacgtaaatc 1549

tggtgtgatt aaactacacg ataaggaaat gaaaaaccgg aatgcgttcg aagccattaa 1609

caatggtttt gccttggtca cggaagaacg tcgctctaca gggatttatg cgaatctcag 1669

tattgagttt aactcattaa tttctaacat gaagaaatcc tatatcagca gttaggtttt 1729

attgagtaac ncaaaaatga aaagcgacac gcaatggggt cattgattcc atgaatgtga 1789

aaacgccatc acaaaaccna tattggntca ntatctgggg tggtaaccaa caaaaagtgg 1849

tcattggtcg ttggttatta acccaccctg aaatcttgat gttagacgaa ccaacacgtg 1909
```

88

gtatcgacat tggtgcgaaa tatgaaattt atcagctgat tatggagtta gccaaaaaag 1969

ataaaggtat catcatgatt tcatctaaag gccagagtta ttaggggtac tgaccgaatt 2029

<210> 38
<211> 166
<212> PRT
<213> Pasteurella multocida

<400> 38
Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln
 1   5   10   15

Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
            20   25   30

Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
        35   40   45

Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
    50   55   60

Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
65   70   75   80

Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
                85   90   95

Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
            100   105   110

Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
            115   120   125

Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
        130   135   140

Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
145   150   155   160

Cys Trp Cys Gly Cys Gly
                165

<210> 39
<211> 2628
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (326)..(766)

<220>
<223> mioC

<400> 39
gtcaactaga gtaaaataga cacacttaat tacattgtag aggaatcctt ttatgtcttt 60

agaaatttta gatcagttag aagaaaaaat taaacaagcg gttgaaacta tccaattact 120

```
tcaattggaa attgatgaat taaaagaaaa aaataaccaa tctcaacaag caaatgacgc 180

attacgcagt gaaaatgaac aactaaagag tgagcaccaa aactggcaag aacgtttacg 240

ctcattatta ggcaaaattg ataacgtata attcacttct tattaaggct tagttttct 300

aagccttatt ttttaggaga aatta atg aaa aca aaa att tgt att atc act   352
                            Met Lys Thr Lys Ile Cys Ile Ile Thr
                             1               5

ggc agt acg ctt ggt ggt gca gaa tat gtt gca gaa cat att gct gaa   400
Gly Ser Thr Leu Gly Gly Ala Glu Tyr Val Ala Glu His Ile Ala Glu
 10              15                  20                  25

ata tta gaa caa caa gat tat cct gta cgt tta gaa cat gga cca aat   448
Ile Leu Glu Gln Gln Asp Tyr Pro Val Arg Leu Glu His Gly Pro Asn
                30              35                  40

ttt gaa gaa gtg atc gat gaa aaa tgt tgg ctt gtt gtc acc tct acc   496
Phe Glu Glu Val Ile Asp Glu Lys Cys Trp Leu Val Val Thr Ser Thr
            45              50                  55

cat ggt gca ggt gaa tta ccg gat aat att aaa cct ctg ttt gaa aaa   544
His Gly Ala Gly Glu Leu Pro Asp Asn Ile Lys Pro Leu Phe Glu Lys
            60              65                  70

tta gca ttt cac cca aaa cag tta gct gac tta cgc ttt gcg gtg atc   592
Leu Ala Phe His Pro Lys Gln Leu Ala Asp Leu Arg Phe Ala Val Ile
        75              80                  85

ggg tta ggt aat tcg gat tat gat acc ttc tgt cac gca gtg gat cat   640
Gly Leu Gly Asn Ser Asp Tyr Asp Thr Phe Cys His Ala Val Asp His
 90              95                  100                 105

gtg gaa caa tta ctg cta agc aaa gat gct tta caa ctg tgt gaa tcg   688
Val Glu Gln Leu Leu Leu Ser Lys Asp Ala Leu Gln Leu Cys Glu Ser
                110             115                 120

cta aga atg gat atg cta acc att act gat cct gaa cac acg gcc gaa   736
Leu Arg Met Asp Met Leu Thr Ile Thr Asp Pro Glu His Thr Ala Glu
            125             130                 135

caa tgg ctc cca caa ttt ctc agt caa tta taatatttat tccctataca   786
Gln Trp Leu Pro Gln Phe Leu Ser Gln Leu
            140             145

atggcatatg taaatcaaat atgccatttt tcatctcgat caagcataat atttaaccaa 846

tcaaatcaat attttctctg tggataacta agatcaaaac tgtataaaag ctgtttttat 906

tccctgaata agattgaatg ttttttattc tgtggataac taaagaagtt attcacagtt 966

ttttctggtg ccaaattgag atcttaacaa cttaaaaaat gatctaagtt attcatttaa 1026

aaaaagaaaa ggatcttaat cacagcacta taggatccta ataatcataa taataagatc 1086

tctttatata aaaagatcct atctttatta actcacgatc tttttcacga tcatcgtaca 1146

gtcttgatca aaaatgtttc tttcatggat ccataaattt cagtagaata gccaaccagc 1206

aaaaaggatc aaaagatcca taaaatccga gataaattaa caaggttact atgtttttata 1266
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90

```
ctgaaaatta tgatgttatt gtgatcggtg gtggacacgc aggtactgaa gctgcacttg 1326

caccggcacg catgggactc aagaccctat tattaaccca taatgttgat acactagggc 1386

aaatgtcttg taatcctgcg attggtggga ttggtaaagg ccatttagtc cgagaaattg 1446

atgcgatggg cggtttaatg gcaactgctg cggaccaagc aggaatccaa tttcgtacct 1506

taaacagcag caaaggaccg gcggtacgtg ctacacgtgc gcaagctgac cgcgtttat 1566

atcgccaagc agtacgtatt gcattagaaa atcaagaaaa tttagatatt tttcaacaag 1626

aagtgaccga tattatttta gatcaggatc gtgtctgcgg tgttgttact aaaatgggtt 1686

taaaatttca cgcaaaagca gtgattttaa cagccggtac tttcctttct ggtaagatcc 1746

acattggttt agaaaattat acaggtggac gcgcgggtga tcctgcttca gtgatgttag 1806

ccgatcgttt aagagaactg aatttacgtg tanatcgttt aaaaacgggt acaccgcccc 1866

gtattgatgc acgtactatt gatttctcaa tactggctaa acaacatggc gatgaaaaat 1926

tacctgtctt ttccttcatg ggatctgttg atcaacaccc acgtcaaatt ccatgtttta 1986

ttacccatac aaatgaacaa acgcatgaag tgatccgtaa taacttacat cgcagcccaa 2046

tgtatgctgg gatcattgaa gggatcggtc cacgttattg cccttctatt gaagataaag 2106

taatgcgttt ttctgagcgt aattctcatc aaatctacct tgaacctgaa gggttgacaa 2166

acaaaacaaa gaaattgcgg atttacaaaa acaagtgcaa gcactgcaag cagatttaag 2226

cgaaatggca agaaaaacc gcaatcaagc gttgattgca ggtggtattg gcggtggcat 2286

tgttgcagtc ggtattgagc tcattcgctt gcaatttggg ggctaactga tggcatttga 2346

tgaaaaaaca cgtgcgctgg ttcgtcgcta ctatgtattt gagtttttat cgcttgagca 2406

atcagcaagt aaagctaaag tctcatttaa caccgcgcga cgctggaaga aagaggcggc 2466

aagcaagggc gatgactggg ataaagtgcg tgatgtacaa gtaatggcgg gcaatgagct 2526

gactgatatc acaaaaggat tgttatcggg ctttattatt caatatcgcg caaccatgga 2586

tgagattcaa aactcggatt taaaagcaca agataaagtc ga            2628
```

<210> 40
<211> 147
<212> PRT
<213> Pasteurella multocida

<400> 40
```
Met Lys Thr Lys Ile Cys Ile Ile Thr Gly Ser Thr Leu Gly Gly Ala
 1               5                  10                  15

Glu Tyr Val Ala Glu His Ile Ala Glu Ile Leu Glu Gln Gln Asp Tyr
                20                  25                  30

Pro Val Arg Leu Glu His Gly Pro Asn Phe Glu Glu Val Ile Asp Glu
            35                  40                  45
```

91

```
Lys Cys Trp Leu Val Val Thr Ser Thr His Gly Ala Gly Glu Leu Pro
     50                  55                  60

Asp Asn Ile Lys Pro Leu Phe Glu Lys Leu Ala Phe His Pro Lys Gln
 65                  70                  75                  80

Leu Ala Asp Leu Arg Phe Ala Val Ile Gly Leu Gly Asn Ser Asp Tyr
                 85                  90                  95

Asp Thr Phe Cys His Ala Val Asp His Val Glu Gln Leu Leu Leu Ser
            100                 105                 110

Lys Asp Ala Leu Gln Leu Cys Glu Ser Leu Arg Met Asp Met Leu Thr
            115                 120                 125

Ile Thr Asp Pro Glu His Thr Ala Glu Gln Trp Leu Pro Gln Phe Leu
    130                 135                 140

Ser Gln Leu
145


<210> 41
<211> 5191
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (3203)..(4255)

<220>
<223> mreB

<400> 41
ctgcagtacc aaccacccaa atgttgtgct tctgctgtaa ttcacgcaaa gtgcgcgcga 60

ggttggttac acggattaat ggcacgactt cagcggcacc acaagctact ttacgtgcga 120

tagcggttaa ttgggcagat ttatcttttg gtactatcac agcacacacg cccgctgcat 180

ccgcagtacg caaacaagca cctaagttat gtggatcagt cacaccatct aacactaata 240

gcaacggatt ggactgattt tgtaaaagcg tatctaaatc tgcttcattc aattctttcg 300

ctggctgaac acgtgccatg atgccttggt gtacttcgcc ctctgctttt ttatcaaggg 360

tttggcgatt aacaaattgg atagtaatac ccaaccgatg aagttcattg agcaaaggtt 420

gtaaacgttt atcgtcgcgc cctttgagtg cataaacttc aattaaacgc tctggcgcgt 480

tgtttaaaaa ggcacttact gcatgaatgc cataaatatt ttcactcatc tactttctct 540

ttttagctga tttcttactg gcttttttcg tggttgttga tggtttaaca acgcttgttt 600

ttcttaccgc acttttactg gtgcttggtt tacgtttatg gcgttgtttt tcgagacttt 660

cagcgtagcg tgcatttttc ttgagcttgt ctttggctgt tttgccttct cgtaatggtt 720

tacgctcact cgacactaaa gaaaaatcca cttggcgttg ttcaaggcta actgcttcca 780

cacggatttt taccttatcg ccaatgcggt agatcatacc actattttca ccgattaaac 840
```

```
gttgtcgagc gagatcaaat tggtagtagt cgttatctaa ggtagaaatg tggactaagc 900

catcaataaa gaggtcatct aagcggacaa ataagccaaa acctgtcaca gatgaaatca 960

cacctgtaaa ttcttcgcct acatgatctt gcatatattc gcattttagc cagtctgcaa 1020

catcacgagt ggcatcatcg gcccgtcgtt ctgtcatgga gcagtggtcg cctaatacat 1080

ccatgtcatc aagtgtatag tgataccctc ccgtatcagt ggttctccgt ttcgagcctt 1140

ttagtttggc taacaagtat ttaatcccac gatgcaaagt caaatcagga taacggcgaa 1200

ttggcgaagt aaaatgcgca tattcttcga gtgcaagccc aaagtgccca atattgtcag 1260

gatgataaac ggcttgactt aacgaacgta atacatggtt tgcaataact catgatctgg 1320

acgttcgcga atttgctcca ataatttagc gtagtctgcg gtacttggtt tactgccacc 1380

ttcaaggctt aaaccacatt cactgaggaa ttggcggaag cccgtcactt tttcttcgct 1440

tggacccgca tgaatacgga aaagggctgg ctcttgatgt ttttccataa agtttgccgc 1500

cgcaatattg gcgaggatca tacattcttc aatgatttta tgcgcatcat tacgaataac 1560

aggctcaatc cgttcgattc gccccatttc attaaacaca aacttacttt caatggtttc 1620

aaagtcaatg gcgccacgtt gatgacgggc ttccactaag gcttggtaca ttacatggag 1680

ttcttttaaa tggggaacca gtgcttgata acgagtacaa agttcttcat cgtcctctaa 1740

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ttcatagcct gtgattttac cttttgctga aacattcagc tcacagacca tacataagcg 1860

atcgacttgt gggtttaatg aacaaagtcc attggagagg atttccggta gcataggaac 1920

aacgcgattt gggaaatata ccgagtttcc acgcgcatgt gcttcggtat caagggcagt 1980

acgtaaacga acatagtagc tgacatcggc aatggcaacc cacagtttcc aaccgcctcc 2040

acgttttttc tggcaaaaaa ccgcatcgtc aaaatcgcga gcatcttcac catcaatggt 2100

gactaacgga agatggcgta aatcaatacg tcctgatttg gcttcttccg gtacttcttc 2160

actcagttta gaaacttgtt tgaggaccgc gtctggaaaa acatggggaa tatcatgatt 2220

acggatagca atttccacct ccatcccttt gccatattt tcaccgagaa tttcgctaat 2280

cattccaaca ggttggctaa atgttgcggt acgtggtttt aattcaacta caaccacttg 2340

tcccatacga gcgccttggc ggtgttcatt cggaattaaa atgtcgcgat taattcgact 2400

atcgtcaggt actacataac caataccatc ttctaagaaa aaacgaccaa caatctgttt 2460

tttacgctgt tgtaagacgc ggacaatccg cacttcttgg cgaccacgac ggtcaaaacc 2520

gctaggttgg gcgaggacat agtcaccgtg cattactcgc tgcatttggc tgttgggtat 2580

aaaccaatcg ctgtctttac cttcgacttg taaaaaacca taaccatcac gatgacctaa 2640

tacggtccct tttaataaat ccagtttttc cggtaaagcg tagcgtttac gtttagtgaa 2700
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93

```
aaccaattgt ccgtcatttt ccatcgctct taagcgacgg cgcatggctt cttgttgttc 2760

ttcattttga atagcaaatg tggtcagtaa ttcttctttt gagataggtg cattatgttg 2820

acgaattgta tcaagaataa attcgcgact tgggatcggg ttctcatatt ttgcgagttc 2880

ttcttgatag tttggatctt gcaaatgtgg attgtttttg atttttgcca taatgactcc 2940

ctttgagaat ggaaatacgc attcgtttaa tgacctcaag tttgacactc tgatttgttg 3000

aaagcaagta aaaaacctgt tcgtgactga aacaatctgt actcgcggga tttgtcgtgc 3060

atgaaagcgt aaagacaaag caaatttcga caatttacag aaaattctct gttataaagg 3120

tacatttttt gatacattta gcacaatttt tcaatactca aatcagagtg tccattattt 3180

aatttagttc agcggaattc tt atg tta ttt aaa aaa att cga ggc tta ttt 3232
                         Met Leu Phe Lys Lys Ile Arg Gly Leu Phe
                          1                 5                  10

tca aat gat ctg tcc atc gat ctt ggc aca gcg aat acc tta att tat 3280
Ser Asn Asp Leu Ser Ile Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr
             15                  20                  25

gtc aaa gga caa ggg att gtt tta gat gaa cct tct gtt gtg gcg att 3328
Val Lys Gly Gln Gly Ile Val Leu Asp Glu Pro Ser Val Val Ala Ile
             30                  35                  40

cgc caa gaa cgt tca ggt gca tta aaa agc att gct gcg gtt ggt cgt 3376
Arg Gln Glu Arg Ser Gly Ala Leu Lys Ser Ile Ala Ala Val Gly Arg
         45                  50                  55

gat gcc aaa tta atg tta ggc cgt aca ccg aaa agc att gca gcg att 3424
Asp Ala Lys Leu Met Leu Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile
     60                  65                  70

cgt cct atg aaa gat ggg gtg atc gca gat ttc ttt gtg aca gaa aaa 3472
Arg Pro Met Lys Asp Gly Val Ile Ala Asp Phe Phe Val Thr Glu Lys
 75                  80                  85                  90

atg ttg caa tat ttt att aaa caa gtg cac agc agc aat ttt atg cgt 3520
Met Leu Gln Tyr Phe Ile Lys Gln Val His Ser Ser Asn Phe Met Arg
                 95                  100                 105

cca agt cca cgt gtc tta gtt tgt gta cct gcg gga gct acg caa gtc 3568
Pro Ser Pro Arg Val Leu Val Cys Val Pro Ala Gly Ala Thr Gln Val
             110                 115                 120

gaa cga cgt gca atc aaa gaa tct gcc att ggt gct ggg gca cgc gag 3616
Glu Arg Arg Ala Ile Lys Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu
             125                 130                 135

gtg tac ttg att gag gaa ccg atg gcg gca gcg att ggt gct aaa tta 3664
Val Tyr Leu Ile Glu Glu Pro Met Ala Ala Ala Ile Gly Ala Lys Leu
     140                 145                 150

cct gtt tcg act gcc aca ggt tcg atg gtg atc gat atc ggt ggt ggt 3712
Pro Val Ser Thr Ala Thr Gly Ser Met Val Ile Asp Ile Gly Gly Gly
155                 160                 165                 170

acg acg gaa gtt gcg gtg att tct tta aat ggc att gtg tat tcc tct 3760
Thr Thr Glu Val Ala Val Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser
```

94

```
tca gtc cgc att ggt ggt gat cgt ttt gat gag gcg att att tct tat   3808
Ser Val Arg Ile Gly Gly Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr
            190             195             200

gta cgc aag acg ttc ggt tca att att ggg gaa ccg aca gca gag cgt   3856
Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg
        205             210             215

atc aaa caa gag att ggt agt gcg ttt att caa gaa ggc gat gaa gtc   3904
Ile Lys Gln Glu Ile Gly Ser Ala Phe Ile Gln Glu Gly Asp Glu Val
        220             225             230

cgt gaa att gaa gtg cat ggt cat aac tta gca gaa ggt gcg ccg cgt   3952
Arg Glu Ile Glu Val His Gly His Asn Leu Ala Glu Gly Ala Pro Arg
235             240             245             250

tct ttc aaa ctc acc tca cgt gat gtg tta gaa gct att caa gcc ccg   4000
Ser Phe Lys Leu Thr Ser Arg Asp Val Leu Glu Ala Ile Gln Ala Pro
                255             260             265

tta aat ggc att gtt gcg gca gtg cgc acg gcc ttg gaa gag tgt caa   4048
Leu Asn Gly Ile Val Ala Ala Val Arg Thr Ala Leu Glu Glu Cys Gln
                270             275             280

cca gaa cat gct gcg gat att ttt gaa cgt ggc atg gtc tta act ggt   4096
Pro Glu His Ala Ala Asp Ile Phe Glu Arg Gly Met Val Leu Thr Gly
            285             290             295

ggc ggt gcc ctt att cgt aat att gat gtt tta ctg tca aaa gaa acc   4144
Gly Gly Ala Leu Ile Arg Asn Ile Asp Val Leu Leu Ser Lys Glu Thr
        300             305             310

ggt gtg ccg gtt atc atc gcc gat gat cct tta acc tgt gtt gcc cgt   4192
Gly Val Pro Val Ile Ile Ala Asp Asp Pro Leu Thr Cys Val Ala Arg
315             320             325             330

ggt ggt ggc gag gca tta gag atg atc gat atg cac ggt ggt gat att   4240
Gly Gly Gly Glu Ala Leu Glu Met Ile Asp Met His Gly Gly Asp Ile
                335             340             345

ttt agt gac gat atc taatatgatt taaaagtgcg gtgatattag accgcacttt   4295
Phe Ser Asp Asp Ile
            350
```

```
tacttctctt ttattgctga caaggctagc ctaattcgta tatgaaacct atttttggaa 4355

aagcacctcc tttaggtctt cgcttaattc tggcgatttt agcatccatt gcattgattg 4415

tttcggacgg tcaatccaat gcgatgatta aagcacgcag tattatggaa accgcagtag 4475

gcgggctgta ttatcttgcc aatacaccga gaacggtatt ggatggggtt tcagataatt 4535

tggttgatac caataaattg caaattgaaa accgagtttt gcgtgatcaa ctgcgtgaaa 4595

aaaatgcaga tttattgttg ttagatcaac tcaaagtaga aaatcaacgc ctgcgcttat 4655

tgcttaattc ccctctacgt acagatgagt ataaaaaaat tgctgaagtt ttaacggcag 4715

aaactgatgt gtatcgtaag caagtcgtga ttaaccaagg acaacgtgac ggtgcttatg 4775
```

```
tcgggcagcc gattattgat gaaaagggta ttgttgggca acttatctcc gttggtgaaa 4835

atacgagtcg cgttcttcta ttgacagatg tgactcattc tattccagta caagtactac 4895

gtaatgatgt ccgtttgatt gctagtggaa caggacggaa tgatgaactg agtttagatc 4955

atgtgccgcg ttcggtcgat attgtcaaag gggatttatt agtcacttct ggattaggtg 5015

ggcgtttttt agaaggttat cctgttgcca ttgtggaatc cgtatcacgt gatgggcaaa 5075

attattttgc tactgtaaca gcaaagccat tagcttcgat tgaacgttta cgctatgttt 5135

tgcttttatg ccgacgaat gaagagatgc gcaaagtcca gtctatttca cctgca     5191
```

<210> 42
<211> 351
<212> PRT
<213> Pasteurella multocida

<400> 42

```
Met Leu Phe Lys Lys Ile Arg Gly Leu Phe Ser Asn Asp Leu Ser Ile
 1               5                  10                  15

Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr Val Lys Gly Gln Gly Ile
                20                  25                  30

Val Leu Asp Glu Pro Ser Val Val Ala Ile Arg Gln Glu Arg Ser Gly
            35                  40                  45

Ala Leu Lys Ser Ile Ala Ala Val Gly Arg Asp Ala Lys Leu Met Leu
        50                  55                  60

Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile Arg Pro Met Lys Asp Gly
65                  70                  75                  80

Val Ile Ala Asp Phe Phe Val Thr Glu Lys Met Leu Gln Tyr Phe Ile
                85                  90                  95

Lys Gln Val His Ser Ser Asn Phe Met Arg Pro Ser Pro Arg Val Leu
                100                 105                 110

Val Cys Val Pro Ala Gly Ala Thr Gln Val Glu Arg Arg Ala Ile Lys
            115                 120                 125

Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu Val Tyr Leu Ile Glu Glu
        130                 135                 140

Pro Met Ala Ala Ala Ile Gly Ala Lys Leu Pro Val Ser Thr Ala Thr
145                 150                 155                 160

Gly Ser Met Val Ile Asp Ile Gly Gly Gly Thr Thr Glu Val Ala Val
                165                 170                 175

Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser Ser Val Arg Ile Gly Gly
                180                 185                 190

Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr Val Arg Lys Thr Phe Gly
                195                 200                 205

Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg Ile Lys Gln Glu Ile Gly
        210                 215                 220
```

96

```
Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His
225             230             235             240

Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser
                245             250             255

Arg Asp Val Leu Glu Ala Ile Gln Ala Pro Leu Asn Gly Ile Val Ala
            260             265             270

Ala Val Arg Thr Ala Leu Glu Glu Cys Gln Pro Glu His Ala Ala Asp
            275             280             285

Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Gly Ala Leu Ile Arg
    290             295             300

Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile
305             310             315             320

Ala Asp Asp Pro Leu Thr Cys Val Ala Arg Gly Gly Gly Glu Ala Leu
                325             330             335

Glu Met Ile Asp Met His Gly Gly Asp Ile Phe Ser Asp Asp Ile
                340             345             350
```

<210> 43
<211> 2172
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(1464)

<220>
<223> pnp

<400> 43
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acc cgc gtt ggg att ggg tgg cac ctg aac cca aat acc gcg tta att   48
Thr Arg Val Gly Ile Gly Trp His Leu Asn Pro Asn Thr Ala Leu Ile
 1               5                  10                  15

gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc gaa gca tac cgt   96
Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
                20                  25                  30

atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct  144
Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
            35                  40                  45

gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc  192
Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
        50                  55                  60

agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc  240
Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
65                  70                  75                  80

gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca  288
Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
                85                  90                  95
```

97

```
gtg gat act gtt cgt gca tta gat att tgt act ggt gtt tta cca cgt    336
Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
            100             105             110

aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct    384
Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala
            115             120             125

gtc gcg aca tta ggt aca gaa cgt gat gca caa att att gat gaa tta    432
Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu
            130             135             140

aca ggt gag cgt tca gat cac ttc tta ttc cac tac aac ttc ccg cca    480
Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro
145             150             155             160

tat tct gtg ggt gaa acc ggt atg att ggt tca cca aaa cgt cgt gaa    528
Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu
            165             170             175

att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct gca gtg atg cca    576
Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro
            180             185             190

aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc tct gaa atc aca    624
Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr
            195             200             205

gaa tca aat ggt tct tct tct atg gca tcg gtt tgt ggt gcg tct tta    672
Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu
            210             215             220

gca tta atg gat gcg ggt gta cca att aaa gcg gcg gtt gca ggt att    720
Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile
225             230             235             240

gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg gtg ctt tca gac    768
Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp
            245             250             255

atc tta ggt gat gaa gat cac tta ggt gac atg gac ttc aaa gtc gcg    816
Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala
            260             265             270

ggt aca cgt acg ggt gtg acg gca tta caa atg gat atc aaa atc gaa    864
Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu
            275             280             285

ggt atc aca gca gaa atc atg caa att gcg tta aac caa gcg aaa agc    912
Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser
            290             295             300

gca cgt tta cac att tta ggt gtg atg gag caa gcg atc cca gcg cca    960
Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro
305             310             315             320

cgt gcg gat att tct gat ttt gca ccg cgt att tac act atg aaa att   1008
Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile
            325             330             335

gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt ggt gca acc att   1056
Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile
```

98

```
cgt gcc tta aca gaa gaa aca ggt acc tca att gat atc gat gat gat   1104
Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp
        355                 360                 365

ggt acg gtg aag att gct gcg gtt gat ggc aat tca gca aaa gag gtg   1152
Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val
        370                 375                 380

atg gcg cgt att gaa gat att act gca gaa gtt gaa gcg ggt gca gtg   1200
Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
385                 390                 395                 400

tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt gcc ttc gtt tct   1248
Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
                405                 410                 415

atc gta ggt aac aaa gaa ggc tta gtg cat att tct caa atc gcg gaa   1296
Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
                420                 425                 430

gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg ggg caa gaa gtg   1344
Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
        435                 440                 445

act gtt aaa gtg gtt gag att gat cgt caa ggt cgt att cgt tta acc   1392
Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
        450                 455                 460

atg aaa gaa gtt gca cca aag caa gaa cac gtt gat tct gtt gtc gca   1440
Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
465                 470                 475                 480

gac gtt gcc gca gaa gaa aac gca taagcaataa acaccaacgc ccttcgtgat   1494
Asp Val Ala Ala Glu Glu Asn Ala
                485

aaagggcgtt ggtgtgcatg ttgataagta caatttgtgc tttaaggcga agcgaaatga   1554

agcaatttca tccgtggtta aagtgcctgc taattttccc attttgggta tgttgtttaa   1614

cagcttgtgt taatcatgaa caagtttttc tttcaaaaga gaaattaatg ttagcagagc   1674

aacatccgaa tgatcatctt gagcatgagg tgatggttgc gcaaattagc gaattgttac   1734

ttgttaaagg gttaaaaaaa gaagaacgtg cgattttaca ttttgagcga ggcgtgctgt   1794

acgatagctt aggattgtgg gcattggcgc gttatgattt tgaccaaaca ttagcgttgt   1854

atccaaagtt ggcagcagcg tttaattatt taggtttata tttattgtta gaggaagatt   1914

acagcgcatc tctagatatc tttaatgtgt tgtttgaact tgatcctcaa tatgagtatg   1974

cattcctaaa tagagggcta aattttt att acgtcggacg ttatgaatta gctcagcggg   2034

attttcttca attttatcaa gccgataaat cagatccata ccgcacttta tggctttatt   2094

taaatgaatt aaagcataat cctcaggatg cttctaaaaa tcttgctcaa cgagcaatgg   2154

ggctttctga tgaatatt                                                 2172
```

<210> 44
<211> 488
<212> PRT
<213> Pasteurella multocida

<400> 44
Thr Arg Val Gly Ile Gly Trp His Leu Asn Pro Asn Thr Ala Leu Ile
1   5   10   15

Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
                20   25   30

Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
            35   40   45

Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
        50   55   60

Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
65   70   75   80

Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
                85   90   95

Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
                100   105   110

Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala
            115   120   125

Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu
        130   135   140

Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro
145   150   155   160

Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu
                165   170   175

Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro
            180   185   190

Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr
            195   200   205

Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu
    210   215   220

Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile
225   230   235   240

Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp
                245   250   255

Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala
                260   265   270

Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu
            275   280   285

Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser
    290   295   300

100

```
Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro
305             310             315             320

Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile
            325             330             335

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile
            340             345             350

Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp
            355             360             365

Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val
        370             375             380

Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
385             390             395             400

Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
            405             410             415

Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
            420             425             430

Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
            435             440             445

Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
        450             455             460

Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
465             470             475             480

Asp Val Ala Ala Glu Glu Asn Ala
            485


<210> 45
<211> 633
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (2)..(631)

<220>
<223> purF

<400> 45
c gat ggg gtt tct gtt tat gct gcc cgt gtt cat atg gga caa cgt tta  49
  Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu
   1               5                  10                  15

ggt gaa aaa att gca cgg gaa tgg gcg gat gtg gat gat att gat gtg  97
Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val
            20                  25                  30

gtc att cct gtg cct gaa acc tct aac gat att gct tta cgt att gcg  145
Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala
            35                  40                  45
```

101

```
cgc gtg tta aat aaa ccg tat cgt caa ggt ttt gtg aaa aat cgc tat    193
Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr
    50                  55                  60

gta gga cgt acg ttt att atg ccg ggg cag gca ttg cga gtc agt tct    241
Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser
65                  70                  75                  80

gtt aga cgt aaa ctc aat acc att gct tca gaa ttt aaa gat aag aat    289
Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn
                85                  90                  95

gtg tta tta gtt gac gac tcg att gta cgt ggt acc acg tct gaa caa    337
Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln
                100                 105                 110

att gtc gaa atg gcg aga gcg gca ggt gcg aag aaa att tat ttt gcc    385
Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
                115                 120                 125

tct gct gca cca gaa att cgt tat cca aat gtg tat ggt att gat atg    433
Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
    130                 135                 140

cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att    481
Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
145                 150                 155                 160

gct aac tta att ggt gtg gat aaa ttg att ttc caa gat ttg gat gcg    529
Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
                165                 170                 175

tta act ggt tct gtg caa caa gaa aat cca agt att caa gac ttt gat    577
Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
                180                 185                 190

tgt tcg gtg ttt aca ggg gtt tat gtg acg ggc gat att aca cct gaa    625
Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu
                195                 200                 205

tat ctg ga                                                         633
Tyr Leu
    210


<210> 46
<211> 210
<212> PRT
<213> Pasteurella multocida

<400> 46
Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu
 1               5                   10                  15

Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val
                20                  25                  30

Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala
            35                  40                  45

Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr
    50                  55                  60
```

102

```
Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser
 65                  70                  75                  80

Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn
                     85                  90                  95

Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln
                100                 105                 110

Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
            115                 120                 125

Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
        130                 135                 140

Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
145                 150                 155                 160

Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
                165                 170                 175

Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
                180                 185                 190

Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu
        195                 200                 205

Tyr Leu
    210


<210> 47
<211> 4788
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(876)

<220>
<223> rci

<400> 47
gac gag gag aga aaa tta gct gat ttg gca aaa ggt atc gct cca gat      48
Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp
 1               5                   10                  15

att att ttt aga gat gta ata gaa cgc tat caa aat gaa gtg tct ata      96
Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
                20                  25                  30

act aaa aaa ggc gcg cga aat gaa att ata aga tta aac cgc ttt tta     144
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
            35                  40                  45

aga tat gat att tct aat ctg tat att cgt gat tta aga aaa gaa gat     192
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
        50                  55                  60

ttt gag gag tgg atc aga att cgc cta acc gaa gta tcg gat gct agc     240
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
```

103

```
gtt aga cgt gag ctt gtt act ata tcg tca gtg ctg aca aca gca ata    288
Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
                85                      90                  95

aat aag tgg gga tat att tca agg cat cca atg act ggt att gaa aaa    336
Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys
            100                     105                 110

cca aaa aac tcg gca gaa aga aaa gaa cga tat tca gaa cag gac att    384
Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile
            115                     120             125

aaa aca ata tta gaa aca gct aga tat tgt gaa gat aaa cta ccc ata    432
Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile
        130                     135             140

aca ctc aaa caa aga gta gca att gca atg tta ttt gct att gaa acc    480
Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr
145                     150                 155                 160

gct atg cgt gct ggt gag att gct agt ata aaa tgg gat aat gtt ttt    528
Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe
                165                     170                 175

ctt gaa aag aga ata gta cat tta ccg aca act aaa aac ggg cac tct    576
Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser
            180                     185                 190

aga gat gtg ccg ctt tcg caa aga gct gtt gcg cta att tta aaa atg    624
Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met
            195                     200             205

aaa gag gta gaa aat gga gat ctt gtg ttt cag acc acg cct gaa tca    672
Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser
        210                     215             220

tta agc acc acg ttt aga gtg tta aag aaa gag tgt gga ctt gaa cat    720
Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His
225                     230                 235                 240

ctc cat ttt cat gat acg aga agg gaa gcg ttg acg aga tta tct aag    768
Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys
                245                     250                 255

aaa gta gat gta atg act cta gcc aaa att agc gga cat aga gat tta    816
Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu
            260                     265             270

aga att tta caa aac aca tat tac gca ccg aat atg agt gaa gtg gca    864
Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
            275                     280             285

aac ttg ttg gat taattcactc ttcttaaata cgcctttgc cacttgatta         916
Asn Leu Leu Asp
    290

catcgccagc cttatatctt ttactttcat tacttccttt ttctaatgaa actggggatg 976

gaaagtcttg gcgggtaata atatgacgag atgtgtaatt gtaagaacga ttaatcatga 1036
```

104

```
tagaaatgtc ttcaatacta agaagaactg gactatcttc tttaagttga gctaaggctc 1096

caaacctcac agagcgtagc acttcatctt gttgtttctt tgttagagaa atattttcca 1156

tttttacctc acttaaataa aaaagccgtc atggacggct taataaagca tttcgctata 1216

cagttctttt gaggtgtacc caatatcgaa cttgatttga ttgttttgtt ttgcgatttc 1276

cagtgcttct tttcgatcaa caaatcttcc gaagttggta ataacaccct gtttcttacc 1336

aattagcgga tattgtgtac cgttctcaat agatttaatt tgtttacgca taaacatgtc 1396

atagtgtctc gcgccagtca ctaaatgaag ttcttttgtt gtgtaatctt caagctcgca 1456

cgcagcgcag acgattaatt ctggacgatc tcccattttc ctatctccga gcatttttca 1516

tagcctcaaa ccaagcttgt gcgtctcctt cactgtaaaa taatgaaccg ctttctagca 1576

tttttctgtg cttatctcta ttagcatcaa aatagaatct aataattgtt gagttacctc 1636

ttttaaagac ctcttgattg tggtgtgctg ttttgattgg agcgggcaaa gtaagcgtta 1696

ctgttgggcg tggttcttcc cacattccga ctatatcaaa tggattttct aaatgcggat 1756

atttgttatg ttcaaaaaaa gaagatccat caatcgtcca agaatttctc tcaaattgtg 1816

tcttgctctt gccaatttga aatacacctt gatataagaa agtgttgaac ggaaagaact 1876

ttgaataatc agcagttaca tatcctttac ttccatttct aagcacaact ggctcaccgg 1936

ttaatgcttt ttctaagtca aatgctttca tttttttactc tccagcttgc tcatcaataa 1996

gctcatcaat ccattctcga atttcagatt ggaaattttc taacgaatta ttttcattaa 2056

aataatctgc ttcttttaac ttactcaccg ctgttttact aaagcattta taaaaaagac 2116

gcttttcttc aaacaaatca tcttttgaga ttgcgcatac ttttcctacg ccctctatac 2176

ttttgtcttg aataaaacta ttaaaaagaa cctcttcttg ctgcttgttt tctactaaaa 2236

tagaaatcgt atattttttt ggatattcca tttttaatcc tttcttttag ataacaaaaa 2296

accgcatttc tgcggttatt ctgtgtattt atttaaaata ttacttatag tttcagcatc 2356

ttctaatgtt aatttagaat agcttgaggt cattttcct ttaacggcaa tcctcaattc 2416

ttccagcttt aagctataca agtagtcttt tttatcttta taaatacgac cgtacaccat 2476

tccggataat ttaccttctt catacccatt agataaattg atctttctat ctcgaccgcg 2536

cactctaatt gttaaatatt ttcttccaat ttttaagact tcagcctcat gttcaatgtt 2596

tgagcgcatg agtgtttcta aaaaatatac ggtatcgcca actttaagat ttttaatcca 2656

atctttattc ataaatacccc ttatactttc ggtggcagtg gaagtggttg ccaatgagtt 2716

actgaagata gatggtaagt acgaagagac ataaagaaaa catcatctcg ccacgcgatt 2776

tttatttccc ctctatctgt ataaatcaga atatcctctc tctcactggg caatctatct 2836

tttacactaa tccagccatc atcttgcgaa aattccacaa tttctggctt ttcaagcacc 2896
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105

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aaatcagagc cgtaatcttc tttttcctct tcgctcaact gcttttcctt gcagtcagcc 2956

ttgccaagga cgacaccgta cacggcataa ggtaaatcat tcaacgcaaa atcctcatga 3016

tcacacatat catctgcgaa ctcatgagct tctactgcac catctaaaca actttgctta 3076

gcttgatnta atgtttcgtg taagttaacg atatgtatgt cattagatac atctactgag 3136

aaaaattttt tttctgtttc tatcatagtt aaattcctta ttcttttatt aatgggcgag 3196

gaatcggttg ccagtgtgta acgttaatag ctagatcata aattggacca ttctgattta 3256

tagctaccca aaaatattca ccatcagcaa tttctcttga tgcaattgcg taatgctcgc 3316

catattcacc ttcacaaaaa gcaatgactg gtgtttcaac ttctggtaac ttgtcatcaa 3376

cactaatcca gttgctatat tcccaatgaa aattaagctt ctcatagcca ttgatgactt 3436

gatctaacgc aggtcttaat tgggtttctc caacaataat atgtgttgtt atcttaatct 3496

ctgggattcc atctattact tcacaccagt ttttttcaat aaagtccaat ctttttttat 3556

ctgctaaaag actttcatat tctgcttttg tgattgttac tgtttctgtc atagttaaat 3616

tcctcatgat aaattccatg tttatttacc tttttctgg cacaaaaaaa cacgctattg 3676

cgtgctgtct tgattgatat aatcaattaa tctaagccca atccatttca taactggaac 3736

agccatactg tttccaattg ctttgtatcg tggagaatca gggcattcat ctattgattt 3796

gttgcgatat gggattttag tgtaatcgtc tggaaatccc tgtaatcttt cacactcacg 3856

cggcgttagt tttctaacaa ctgattctac tgataaagca acgcaaggaa cattattacc 3916

accagttccc attcttgctt ttaaggttgg tgaaatatca tcgtgaatac gacaagcttc 3976

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agcaagaact ccaccgcttg ctcttaatgt tcccgcaaca tcggatttgc gatattgagc 4156

aaagcttgtc tcaataaagg cggcaatatc ttttgcctgc gttccgctct gttcaatatt 4216

ccctcgcacg cttttggact caatgagtat ttgtgcaaca cttcgttttc tagcacttgc 4276

cacaagaaac actcttttac gacgttgggc aactccgaag tattgagcat cgagaactcg 4336

ccagcagatt gttcggattg aatgcacata accagcgttc gtccatcttc tccctgtgtg 4396

ctgcaatggc tcacactctt gaaccagtcc agccagaagg tgtccgaatg cgttgtccga 4456

ggtggatagc acacccggaa cgttttccca cacgagaatg cacggtggtt tgttgtcatt 4516

gaatctaaca tagtcgatcg cttctaaaat tttaattaaa actaacgtga gatttcctcg 4576

ctcatcgtct aaactttgac gattgccagc aactgaaaaa gattgacaag gagtaccacc 4636

aactaaaacg tctggtgccg gaatttcacg atctaatatt ttctgttgca attcagtcat 4696

atcaccaaga ttgggaacgt tagggtaatg gtaagctaat actgcgcttg ggaattgctc 4756
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106

aattttcagaa aaccagagtg gctctgcgaa tt   4788

<210> 48
<211> 292
<212> PRT
<213> Pasteurella multocida

<400> 48
Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp
  1   5   10   15

Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
               20   25   30

Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
           35   40   45

Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
       50   55   60

Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
 65   70   75   80

Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
                   85   90   95

Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys
               100   105   110

Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile
           115   120   125

Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile
       130   135   140

Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr
145   150   155   160

Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe
               165   170   175

Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser
               180   185   190

Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met
           195   200   205

Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser
           210   215   220

Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His
225   230   235   240

Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys
               245   250   255

Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu
               260   265   270

Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
           275   280   285

107

Asn Leu Leu Asp
    290

<210> 49
<211> 1618
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (2)..(1195)

<220>
<223> sopE

<400> 49
g ggc gat cta tgt ctg aaa ata tct aca tgg tgt caa agt cac aga atc   49
  Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile
  1   5   10   15

aat caa gca att cgc aca att caa agt cta tca acc gca gtc atc ggt   97
Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly
            20   25   30

att gtc tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat   145
Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn
        35   40   45

gaa ccc gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga   193
Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly
    50   55   60

aaa caa ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc   241
Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val
65   70   75   80

aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac   289
Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp
                85   90   95

gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc   337
Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile
                100   105   110

aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa   385
Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys
            115   120   125

aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac   433
Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp
    130   135   140

aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac   481
Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn
145   150   155   160

gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg   529
Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala
                165   170   175

gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg   577

108

```
Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met
        180                 185             190

ggc gat ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac     625
Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp
        195                 200             205

tat gcc gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa     673
Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu
        210                 215             220

cag ggc tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc     721
Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser
225                 230             235                 240

ggt gtc aca caa cca ctc tat ttt gac att aac gac agc tcg act gat     769
Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp
                245             250                 255

gtg aac tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat     817
Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
                260             265                 270

ggc ttt cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc     865
Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
        275                 280             285

aag ttt gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att     913
Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
        290                 295             300

gca ggg gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta     961
Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
305                 310             315                 320

gtg aaa gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc     1009
Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
                325             330                 335

aca aaa ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt     1057
Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
                340             345                 350

aac agt gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat     1105
Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
                355             360                 365

tat cac cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att     1153
Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
        370                 375             380

tct gat gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg             1195
Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385                 390             395

taaggggtag aaaatggctt taccacgcaa acttaaattg atgaatttaa tcatcgacgg 1255

taacaaatat ctcggcgaag tcacggaagt gactcaacca aaattagcaa tgaaaatcga 1315

agaatttcgc gcgggcggta tgattggttc ggtggatgtc aatctcgggc ttgaaaagct 1375

cgaagcggaa tttaaagccg gtggctacat ggtcgaatta attaaaaaat tcggcgggtc 1435
```

109

```
aatcaacggc attccattgc gttttcttgg ctcatatcag cgtgatgaca cagaagaagt 1495

cacatctgtt gagcttgtga tgcaaggtcg atttactgaa attgacagcg gaaacagcaa 1555

agtgggcgat gacactgaac aaacattcaa agtgccttta acgtattaca aaatcattgt 1615

tga                                                               1618
```

<210> 50
<211> 398
<212> PRT
<213> Pasteurella multocida

<400> 50

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Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile
 1               5                  10                  15

Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly
            20                  25                  30

Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn
            35              40                  45

Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly
    50                  55                  60

Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val
65                  70                  75                  80

Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp
                85                  90                  95

Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile
            100                 105                 110

Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys
            115                 120                 125

Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp
    130                 135                 140

Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn
145                 150                 155                 160

Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala
                165                 170                 175

Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met
            180                 185                 190

Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp
            195                 200                 205

Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu
    210                 215                 220

Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser
225                 230                 235                 240

Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp
                245                 250                 255
```

110

```
Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
         260               265               270

Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
         275               280               285

Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
         290               295               300

Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
305               310               315               320

Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
         325               330               335

Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
         340               345               350

Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
         355               360               365

Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
         370               375               380

Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385               390               395
```

<210> 51
<211> 353
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(351)

<220>
<223> unknown C1

<400> 51
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atg aca tta ttt gat gaa tgt aaa tta gct ctt aga gac gat ttt aat     48
Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
  1               5                  10                  15

cta att tgt gat gaa gag aag gat tgt gta atg gat aag ttt tat ttc     96
Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
             20                  25                  30

tat ttc ttg gaa aag aaa gag gaa ttt aat ttt caa gat tat tca ttt    144
Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
         35                  40                  45

gaa gaa atg tat ata ttt tca aaa atg gaa cct gtg tat gtt tta tgt    192
Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
     50                  55                  60

gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc    240
Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65                  70                  75                  80

aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta    288
```

111

```
Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
            85                  90                  95

gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga    336
Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
            100                 105                 110

gtc atc tat aaa aga ta                                             353
Val Ile Tyr Lys Arg
            115


<210> 52
<211> 117
<212> PRT
<213> Pasteurella multocida

<400> 52
Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1               5                  10                  15

Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
            20                  25                  30

Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
            35                  40                  45

Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
        50                  55                  60

Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
    65                  70                  75                  80

Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
            85                  90                  95

Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
            100                 105                 110

Val Ile Tyr Lys Arg
            115


<210> 53
<211> 509
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(507)

<220>
<223> unknown C2

<400> 53
atg aaa aat ttt agg aat ata aat att tat agt gat tat gga aag gtt    48
Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
 1               5                  10                  15

gat aag gaa att ata tta gaa ttc gaa aat gaa ttt aat ata aag ctt    96
Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
```

112

```
cct tct tta tac ata gat tta att acg gcg cat aat gct ccg aag agt    144
Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
            35                  40                  45

gaa gag aat tgc ttt gaa tat tac aat gag cgt aat gag ccc acg ttt    192
Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
    50                  55                  60

tct tcc ttt gga ttt gaa ggg ttt gag aca gag cgg tct agc gcc tct    240
Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
65                  70                  75                  80

ctt gaa aat ata tat gct cag tat att tat gat gat cca atc tat ggt    288
Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
                85                  90                  95

tat gaa cat gtg tat tct ttt ggt agt act ggc gag gga cat ttt atc    336
Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
                100                 105                 110

tgt ttt gat tat cgt gat gat cca aaa ggt gat gaa ccc aaa atc tgt    384
Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
            115                 120                 125

atc gtg att cac gat gaa tat gat gaa aaa aca ggg aaa atg cga ctg    432
Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
    130                 135                 140

ttt cct ata gca gag aat ttt gaa gcg ttt tta gat agt ttg aaa tca    480
Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
145                 150                 155                 160

ttt gat gaa atg ata gag aag tat tcg ta                            509
Phe Asp Glu Met Ile Glu Lys Tyr Ser
                165
```

<210> 54
<211> 169
<212> PRT
<213> Pasteurella multocida

<400> 54

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Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
  1               5                   10                  15

Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
            20                  25                  30

Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
            35                  40                  45

Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
    50                  55                  60

Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
65                  70                  75                  80

Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
                85                  90                  95
```

113

```
Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
            100                 105                 110

Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
            115                 120                 125

Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
            130                 135                 140

Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
145                     150                 155                 160

Phe Asp Glu Met Ile Glu Lys Tyr Ser
                165


<210> 55
<211> 443
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(441)

<220>
<223> unknown C3

<400> 55
atg ata aaa tat tta gag gga aat att aac tcg ttt ata tcg gca tta     48
Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu
1               5                   10                  15

ggt aaa aac gaa agt aat aaa gat att tta aaa tta gta gaa ata gtt     96
Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val
                20                  25                  30

tct tca gat ttt gaa gtg gat gaa cta agt cat aaa gat gaa cac gag    144
Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
            35                  40                  45

ata tat tat ttg ttt tat aag agg ggt gtt gaa ttt tgt ttt aaa aga    192
Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
    50                  55                  60

ata gat gaa gag tat gtc tta tat tcg gtt ttc ttt ttc ttg gta gag    240
Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu
65                  70                  75                  80

gtt gat aat tat ttt tca tgc cca ttt att cat gaa tta ata tgt gat    288
Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
                85                  90                  95

ctt aaa cac gga ttc tca ata gag gat att ata agg ttt tta ggg gag    336
Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
            100                 105                 110

cca aat ttt aaa ggt agt ggc tgg gta aga tat tct tat aat gga aga    384
Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
            115                 120                 125

aat att cat ttc gaa ttt aat gaa tct aat gaa tta tcc cag att agc    432
```

114

Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser
   130   135   140

att ttt att ta   443
Ile Phe Ile
145

<210> 56
<211> 147
<212> PRT
<213> Pasteurella multocida

<400> 56
Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu
  1   5   10   15

Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val
      20   25   30

Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
      35   40   45

Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
   50   55   60

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115

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116

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117

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119

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120

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121

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Met Lys Lys Leu
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122

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Gly Lys Ile Ser Gln Thr Ser Arg Lys Leu Thr Ile Arg Tyr Trp Ile
        295                 300                 305

acg ggt aat aat aca cct tgg aaa ttt aat gct ggg aga tgg gag aga    3657
Thr Gly Asn Asn Thr Pro Trp Lys Phe Asn Ala Gly Arg Trp Glu Arg
        310                 315                 320

agt aca gtg tct ttc cag gag cat tat aaa ggc tat tat gac aaa ttc    3705
Ser Thr Val Ser Phe Gln Glu His Tyr Lys Gly Tyr Tyr Asp Lys Phe
325                 330                 335                 340

cat tct tca act tgt aga ggc tca ggg agc tct aga act tgt caa att    3753
His Ser Ser Thr Cys Arg Gly Ser Gly Ser Ser Arg Thr Cys Gln Ile
                345                 350                 355

gat gca aat cct aag aaa att atg gat tat gca cta aaa att aat gac    3801
Asp Ala Asn Pro Lys Lys Ile Met Asp Tyr Ala Leu Lys Ile Asn Asp
                360                 365                 370

tgg acg aca att aga gaa tta ttt aat act tat ata gat gta agt ggg    3849
Trp Thr Thr Ile Arg Glu Leu Phe Asn Thr Tyr Ile Asp Val Ser Gly
        375                 380                 385

acg att gac caa att tcc cag ttt gat ggt tca aac aga cgt tat gat    3897
Thr Ile Asp Gln Ile Ser Gln Phe Asp Gly Ser Asn Arg Arg Tyr Asp
        390                 395                 400

atg gtg ttt act gat gaa gaa cgg tgt ctt ggc gga aat att ggt aga    3945
Met Val Phe Thr Asp Glu Glu Arg Cys Leu Gly Gly Asn Ile Gly Arg
405                 410                 415                 420

aga aca act cga gct tgg ttt gat caa aaa aat aaa gat att aca aga    3993
Arg Thr Thr Arg Ala Trp Phe Asp Gln Lys Asn Lys Asp Ile Thr Arg
                425                 430                 435

gag ttg aat att gtt cgt cct tct ggt tgg act tct gca tct tcg ggg    4041
Glu Leu Asn Ile Val Arg Pro Ser Gly Trp Thr Ser Ala Ser Ser Gly
                440                 445                 450

ctt ctt gtt gga gct aat atc atg atg gac gag aat aag aat cct gat    4089
Leu Leu Val Gly Ala Asn Ile Met Met Asp Glu Asn Lys Asn Pro Asp
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123

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gcg caa cct tcg aaa ctc ggg aca aat att caa cgt gtt atc tta gta    4137
Ala Gln Pro Ser Lys Leu Gly Thr Asn Ile Gln Arg Val Ile Leu Val
    470                 475                 480

tta tct gat ggt gaa gat aac tgg cca act tat agt aca tta acg act    4185
Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser Thr Leu Thr Thr
485                     490                 495                 500

ctt tta aac aat ggt atg tgt gac aaa att cga gaa caa ttg ggc aag    4233
Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu Gln Leu Gly Lys
                505                 510                 515

tta caa gat cca aat tta cga gag tta cca gga aga att gcg ttt gtt    4281
Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg Ile Ala Phe Val
                520                 525                 530

gcg ttt ggc tat agt cca cca gca aac caa gtt gcc gct tgg aaa aaa    4329
Ala Phe Gly Tyr Ser Pro Pro Ala Asn Gln Val Ala Ala Trp Lys Lys
            535                 540                 545

tgt gta ggt gat caa tat tat acg gct tat tcg aaa gaa gag ttg tta    4377
Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys Glu Glu Leu Leu
    550                 555                 560

gat agt ttc aaa caa att att gga ttt gaa gaa gag gtg ggg cgt tct    4425
Asp Ser Phe Lys Gln Ile Ile Gly Phe Glu Glu Glu Val Gly Arg Ser
565                 570                 575                 580

tca tct cat aaa ccg aaa ttt taagattgtc caaggataac gctaaaaat      4476
Ser Ser His Lys Pro Lys Phe
                585

ctcttagcac aggctaagag attttttat gtgtttttca aattttatct actggtgatt 4536

ttaattcatt acataacata acttttcgt gaataataca gaatagacaa caataagaat 4596

taaaacgctc aaggcataga ggcttagtcg aacaaactaa gctattttgc gcgattgatt 4656

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cgtaataaag tagaagcgat ttttcttttg gctgaaaggt ggtgttagcc tttttcggct 4776

aaagaaaata gtagcaacgg caatataaag ggcgataaag agcattttgt aaatgaacca 4836

tgttgttaca ttttgctgaa aaagaagaaa tagcccaatt cccgaacaga acaacagcgt 4896

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actttcgctc gcatcactct caatgtcttc ttcatcgaca tcacaaacga gttgtaatcc 5196

aaccagtgtt tcactttcac ttgttcggat gagacgtact ccttgtgtat ttcgaccgat 5256

aatattgatt tcgtttacgc gagtacgtac tagcgtaccg gcatcagtaa tgagcataat 5316
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124

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ttgatcgctt tcctcaactt gtgttgctgc aacgacttta ccgttacgct cactcacttt 5376

aatcgagatc acgcctttgg tgttacgtga tttagttggg tattccgcta attcagtacg 5436

tttaccataa ccgttttgtg tggcggttaa aatggcgcct tcattttttg gaataacaag 5496

tgacacgact ttatcaatat tgagatccaa ggcatcatta gtattctcat cagagatctc 5556

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gcgtacacct gttgctgcac gccccatggc acgcacagca ttttcactaa agcgaactac 5676

acgtccttgt gcggagaaga gcatgatttc attttgacca tcggtgatat ccacaccgat 5736

aagttcgtct tcatcacgca agttgagtgc aataatgcct gttgaacgag gacgactgaa 5796

tt                                                                5798
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<213> Pasteurella multocida

<400> 59

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Ala Phe Pro Leu Leu Val Leu Ile Gly Phe Thr Val Asp Gly Thr Gly
        35                  40                  45

Val Val Leu Asp Lys Ala Arg Leu Ala Gln Gly Met Asp Gln Ala Ala
    50                  55                  60

Leu Ala Leu Val Ala Glu Asn Asn Asp Tyr Arg Glu Asn Lys Lys His
65                  70                  75                  80

Gly Asp Val Asn Arg Gln Val Val Ser Pro Gln Asp Lys Ala Lys Phe
                85                  90                  95

Gly Gly Asn Glu Phe Met Ala Lys Gln Glu Lys Arg Asn Gln Glu Leu
            100                 105                 110

Ile Gln Gly Ile Ala Lys Leu Tyr Leu Arg Ser Glu Asn Ala Asn Ala
            115                 120                 125

Ser Ser Asp Ala Pro Ile Thr Ile Asp Lys Pro Phe His Tyr Ser Cys
    130                 135                 140

Glu Glu Leu Asp Leu Pro Thr Ala Asn Glu Tyr Ala Arg Arg Lys Pro
145                 150                 155                 160

Ile Val Cys Glu Val Gln Gly Gly Val Asn Arg Lys Phe Trp Leu Pro
                165                 170                 175

Val Ser Glu Ser Leu Val Ser Glu Asp Lys Leu Lys Lys Asp Arg Val
                180                 185                 190

Arg Leu Glu Ser Asp Thr Ser Tyr Ala Ile Lys Glu Lys Gly Ile Val
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125

Ile Pro Val Glu Leu Met Leu Val Ser Asp Tyr Ser Gly Ser Met Asn
        210   215   220

Ser His Leu Gln Asp Lys Asn Gly Arg Ser Leu Gly Lys Ala Lys Ile
225   230   235   240

Thr Ile Leu Arg Glu Val Val Ser Glu Ile Ser Lys Ile Leu Leu Pro
                245   250   255

Glu Asp Val Ser Glu Gly Val Ser Pro Phe Asn Arg Ile Gly Phe Thr
                260   265   270

Thr Phe Ser Gly Gly Val Arg Gln Arg Asp Val Thr Glu Gly Cys Val
            275   280   285

Leu Pro Tyr Glu Gly Lys Ile Ser Gln Thr Ser Arg Lys Leu Thr Ile
    290   295   300

Arg Tyr Trp Ile Thr Gly Asn Asn Thr Pro Trp Lys Phe Asn Ala Gly
305   310   315   320

Arg Trp Glu Arg Ser Thr Val Ser Phe Gln Glu His Tyr Lys Gly Tyr
                325   330   335

Tyr Asp Lys Phe His Ser Ser Thr Cys Arg Gly Ser Gly Ser Ser Arg
            340   345   350

Thr Cys Gln Ile Asp Ala Asn Pro Lys Lys Ile Met Asp Tyr Ala Leu
        355   360   365

Lys Ile Asn Asp Trp Thr Thr Ile Arg Glu Leu Phe Asn Thr Tyr Ile
    370   375   380

Asp Val Ser Gly Thr Ile Asp Gln Ile Ser Gln Phe Asp Gly Ser Asn
385   390   395   400

Arg Arg Tyr Asp Met Val Phe Thr Asp Glu Glu Arg Cys Leu Gly Gly
            405   410   415

Asn Ile Gly Arg Arg Thr Thr Arg Ala Trp Phe Asp Gln Lys Asn Lys
        420   425   430

Asp Ile Thr Arg Glu Leu Asn Ile Val Arg Pro Ser Gly Trp Thr Ser
        435   440   445

Ala Ser Ser Gly Leu Leu Val Gly Ala Asn Ile Met Met Asp Glu Asn
    450   455   460

Lys Asn Pro Asp Ala Gln Pro Ser Lys Leu Gly Thr Asn Ile Gln Arg
465   470   475   480

Val Ile Leu Val Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser
            485   490   495

Thr Leu Thr Thr Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu
            500   505   510

Gln Leu Gly Lys Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg
            515   520   525

126

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Ile Ala Phe Val Ala Phe Gly Tyr Ser Pro Pro Ala Asn Gln Val Ala
    530                 535             540

Ala Trp Lys Lys Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys
545             550             555             560

Glu Glu Leu Leu Asp Ser Phe Lys Gln Ile Ile Gly Phe Glu Glu Glu
            565             570             575

Val Gly Arg Ser Ser Ser His Lys Pro Lys Phe
            580             585


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<222> (698)..(1468)

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ttattattat caggcctata ttatttatat gcagtaaaaa acgattcaaa ttttgtcata 180

ggtttatcta ttattttagt ttttattatt gtcattccag ggattttgac aaatgctatt 240

ttgaaagcta aggtgaaaaa aatcatggta gatttaccag gttttattga cttagttgca 300

gtaaatgttc aaacagggat tagtattgat gcggctttaa aacaagtggc aatcgatttt 360

aagaaactta atccagatct tacttatgtg atgttaagga ttattagaaa atctgaactt 420

acgggattat cacaagcgtt acaggatctt cgatctcat tgccaacaac agaaataaga 480

atgttttgta ctgttttaca acagagttta aattttggtt cttcaattta ttctcactta 540

attcagttgt ctgcagatat cagggagata caattattaa tcattgagga aaagttaggt 600

acattatcag ctaaaatgag tatcccattg attttgttta ttatgttccc aataatcatt 660

ttaattctag caccaggtat aatgagggta tttccaa atg ttt ttt aaa ttt acc 715
                                        Met Phe Phe Lys Phe Thr
                                          1                   5

aag aaa atc gtt ttt gtt agt tta gct tta tct gtc gtt ggt tgt tct 763
Lys Lys Ile Val Phe Val Ser Leu Ala Leu Ser Val Val Gly Cys Ser
            10              15                  20

acc cat tct cag caa ggc atg aca cag aaa agt atg tca tct gaa aca 811
Thr His Ser Gln Gln Gly Met Thr Gln Lys Ser Met Ser Ser Glu Thr
        25              30                  35

ata acg gca aaa gag act tta tat gaa agt acg caa aat tat tcg gca 859
Ile Thr Ala Lys Glu Thr Leu Tyr Glu Ser Thr Gln Asn Tyr Ser Ala
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127

ctc att tca ctg tat cgc gat gtg ttg aaa gcc aaa gaa gat cct tca   907
Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys Ala Lys Glu Asp Pro Ser
55   60   65   70

ata cgc tat aaa tta gcg aag aca tac tat cag cga ggt gac agc aaa   955
Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr Gln Arg Gly Asp Ser Lys
                75   80   85

tct tct tta ctt tat tta acg cca tta ctg aat gat aat acg aag ctt   1003
Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu Asn Asp Asn Thr Lys Leu
                90   95   100

gct aca caa gcg aaa ata tta cag ata aaa aat cta att caa tta aat   1051
Ala Thr Gln Ala Lys Ile Leu Gln Ile Lys Asn Leu Ile Gln Leu Asn
                105   110   115

aat ttc caa gaa gca att tct gtc gca aat gaa ctc tta tta aaa tca   1099
Asn Phe Gln Glu Ala Ile Ser Val Ala Asn Glu Leu Leu Leu Lys Ser
        120   125   130

cct aat gaa gga gaa gta tat aat tta aga ggt atc gct tat gcg caa   1147
Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg Gly Ile Ala Tyr Ala Gln
135   140   145   150

aat ggg aat ttg gtg aat gcc cga aat gat atc aat aaa gca aga gag   1195
Asn Gly Asn Leu Val Asn Ala Arg Asn Asp Ile Asn Lys Ala Arg Glu
                155   160   165

ttc ttt att aat gat aat gtt gct att aat aat tta gcc atg cta aat   1243
Phe Phe Ile Asn Asp Asn Val Ala Ile Asn Asn Leu Ala Met Leu Asn
                170   175   180

att att aat ggc gat ttt aat aat gct gtt tct tta ctg ttg cca caa   1291
Ile Ile Asn Gly Asp Phe Asn Asn Ala Val Ser Leu Leu Leu Pro Gln
                185   190   195

tat tta aat ggc gtt aag aat tct cga ttg att cat aat ctt gtt ttt   1339
Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu Ile His Asn Leu Val Phe
        200   205   210

gct tta gtt aaa aat ggt gat ctt gat tat gca aaa gat atc att gtt   1387
Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr Ala Lys Asp Ile Ile Val
215   220   225   230

aaa gag cgt tta aat act tca cca gat gat tta att aat gca ttg aaa   1435
Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp Leu Ile Asn Ala Leu Lys
                235   240   245

aaa act aca cat gta tca aaa ggt gta act cgg taacactaag gatttgatat 1488
Lys Thr Thr His Val Ser Lys Gly Val Thr Arg
                250   255

gaaaaagttt ctatcaaata taaaaggaac ctcgtcaatt gaatttgctt tgacgatagc   1548

gttctattta tttgttgtga tgtttatttt tgaattttgt cgattagcgg ttgcgacagc   1608

ttattgggat ttagctataa cggaaagtgt cagaattgcg aagaatgaac aagcaatttc   1668

tggaaattat gaagaagcat ttaggaaagc tcttacaaag caaaaaaaat tccatgatga   1728

128

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atcgacaatt ggatatttgg cgttgttaga agataataaa tttgatgtaa aagtccaata 1788

tgtggattgt gataaagaaa cggaatgtat taaaaatctt ctgcttaata aatttcgcca 1848

accacaaaaa aatcataaag gagagttaat ctctcctacg gggagtcgcg cgactttagc 1908

acaatattct ttaacttata aatataagtt tatggtgccg ttagtatta ttcctgagtc 1968

ttggtctcaa gtagtgctga accgtgaatt tgttgttgta caggaatttg agcgttctca 2028

atttatgtta ggagcaaaac caagttctct tgggacgaat ccatagaaaa tttactcatt 2088

atttcgagct atatatgaaa gagtcaggtt tagttaaatt caagcatttt tggaaaaata 2148

aaaagggcgc agtgacgata gagttccttt ttatgtcaat gtttctgatt gtgctatttg 2208

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129

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acttatatag atgtaagtgg gacgattgac caaatttccc agtttgatgg ttcaaacaga 3888

cgttatgata tggtgtttac tgatgaagaa cggtgtcttg gcggaaatat tggtagaaga 3948

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130

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ggagaagagc atgatttcat tttgaccatc ggtgatatcc acaccgataa gttcgtcttc 5748

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<211> 257
<212> PRT
<213> Pasteurella multocida

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            20   25   30

Ser Met Ser Ser Glu Thr Ile Thr Ala Lys Glu Thr Leu Tyr Glu Ser
        35   40   45

Thr Gln Asn Tyr Ser Ala Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys
    50   55   60

Ala Lys Glu Asp Pro Ser Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr
65   70   75   80

Gln Arg Gly Asp Ser Lys Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu
                85   90   95

Asn Asp Asn Thr Lys Leu Ala Thr Gln Ala Lys Ile Leu Gln Ile Lys
            100   105   110

Asn Leu Ile Gln Leu Asn Asn Phe Gln Glu Ala Ile Ser Val Ala Asn
        115   120   125

Glu Leu Leu Leu Lys Ser Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg
    130   135   140

Gly Ile Ala Tyr Ala Gln Asn Gly Asn Leu Val Asn Ala Arg Asn Asp
145   150   155   160

Ile Asn Lys Ala Arg Glu Phe Phe Ile Asn Asp Asn Val Ala Ile Asn
                165   170   175

Asn Leu Ala Met Leu Asn Ile Ile Asn Gly Asp Phe Asn Asn Ala Val
            180   185   190

Ser Leu Leu Leu Pro Gln Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu
        195   200   205

Ile His Asn Leu Val Phe Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr
    210   215   220

Ala Lys Asp Ile Ile Val Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp

131

Leu Ile Asn Ala Leu Lys Lys Thr Thr His Val Ser Lys Gly Val Thr
                245   250   255

Arg

<210> 62
<211> 1788
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<222> (1)..(600)

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 1   5   10   15

aaa gat gac acc agt ttt gtg act gaa gga aat aac ttt atc aca gca   96
Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
            20   25   30

aaa gac aac tta gaa atc acg gca aaa aat gtt caa att gat caa gcg   144
Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
        35   40   45

aaa aat att caa tta aac gcg aat atc acg atc aat acc aag tct ggt   192
Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
    50   55   60

ttt gtg aat tac ggt acc tta gca agt gct caa aat tta acg att aat   240
Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
 65   70   75   80

acc gaa caa ggc agc att tat aac ata ggc ggt atc ttg ggg gcg ggt   288
Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly
                85   90   95

aaa agt ttg aat ctg agc gcg aaa aga gga gaa aac caa gga gga tat   336
Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr
            100   105   110

ctt att aat caa ggt aag agt cta ctc cat tct gaa ggc gcc atg aac   384
Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn
            115   120   125

ctc aca gcg gat cgc acg gtg tac aat tta ggg aat att ttt gct aaa   432
Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys
        130   135   140

ggt gac gcg acg atc aat gca aac gcg tta att aat gat gtt act ctc   480
Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu
145   150   155   160

132

```
aca ggt cgt ctt gag tat caa gat ctg aaa aaa gat tat acg cgt tat    528
Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr
            165             170             175

tat cgt atc aat gaa acg gca aaa cat ggt tgg cat aat aac ttc tat    576
Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr
            180             185             190

gaa tta aac gtc gac aga gtt tct tgatttgtgc atcaattttg taaccaccgg    630
Glu Leu Asn Val Asp Arg Val Ser
            195             200

ttaataaaac accagcaatt tcaacgccat tcatggcaga taatgccgct gcgacgatca    690

catcaggacg atccgcggaa gtgacaagta aacttccaac gcggaaatgt tccaccatat    750

tggtcaaatt acgtgcacag aaagtgatgc cacgaatgcg acgttcattg atcgcgcctt    810

catgaataat ggcagcacct aaatgtttgg ctaaatcaat ggcacgagtc gcaattaatt    870

ctgcgctcca aggaatacat gccaagattt taattgggct tttctcaaat aaatgataaa    930

tctcagatac ttgattttgt gtgtgttgga aagaatcaaa aatttctgcc aagtcagggc    990

gagtacgacc agattcatca atcggcgcat taaatttatt gatcacaaca ccaagtaaat    1050

tagggttatt tttgctgcca ataatgagg ctgcggcttt gatgcgttct ttgagttctg      1110

ccggtgtttc cgtcgccggt gctgcaacaa gaatgatttc cgcatcaagt gcttgagcaa      1170

tttcatagtt aatgctattg gcataagaat gcttacgcgt agggattaaa ccttccacca      1230

cgacaatttc attgtttttg gcgagttgtt gatgattttc aacaatttt tctagtacca      1290

catcagattg attttgaccg atgagtgatt cagctacact taacataaat ggttcactgg      1350

tttcaatggt ggtactggtg cgaataattg atgttgtgcg atcaatcata tcttcacctg      1410

agttcggctg agaaattggt ttcataaagc cgactttcgc cccttttttgc tccagtgcat      1470

gtgttaaacc taagctgaca ctggttaagc ctacaccagc actaatcggg ataaggataa      1530

ttgtacgtga cataataaac cctaatttgt tgataattta tacaaaaaga aactgccgat      1590

gaatcggcag ttaattgatc tttacgcgat gcaaaggcgc gcggtatctt gtgcaataac      1650

aagttcttca ttcgttggga tcaccatggc aacaggcgta ttgtctgctg taatcacccc      1710

ttcatgacca aagcgagccg ctttgttttt atctgaatcc acttgataac cgaacagttt      1770

taaatggttt aaggttga                                                   1788


<210> 63
<211> 200
<212> PRT
<213> Pasteurella multocida

<400> 63
Val Asn Thr Gly Leu Ile His Ser Asn Gly Asn Ala Lys Leu Thr Phe
 1               5                   10                  15
```

133

```
Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
            20                  25                  30

Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
        35                  40                  45

Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
    50                  55                  60

Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
65                  70                  75                  80

Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly
                85                  90                  95

Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr
        100                 105                 110

Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn
        115                 120                 125

Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys
    130                 135                 140

Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu
145                 150                 155                 160

Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr
            165                 170                 175

Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr
        180                 185                 190

Glu Leu Asn Val Asp Arg Val Ser
        195                 200


<210> 64
<211> 278
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (108)..(278)

<220>
<223> unknown 0

<400> 64
gaattccaac caaatctcac accagagcaa gaacgctaca tagtggaatg gttggcagaa 60

cattacccaa atggaaataa accttaacca tagcaagaga gaagaaa atg aaa att    116
                                                    Met Lys Ile
                                                      1

act att aca cga aat cat cca gaa gta ttt caa gaa tcc gct cgt tta   164
Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu
      5                  10                  15

gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg   212
Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu
```

134

```
gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa    260
Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu Glu
              40                      45                  50

agc aaa agg gga cat agt                                            278
Ser Lys Arg Gly His Ser
            55
```

<210> 65
<211> 57
<212> PRT
<213> Pasteurella multocida

<400> 65
```
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
 1               5                   10                  15

Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
            20                  25                  30

Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
          35                  40                  45

Glu Glu Glu Ser Lys Arg Gly His Ser
      50                  55
```

<210> 66
<211> 1020
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(597)

<220>
<223> unknown P

<400> 66
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gtc aac aca tca aaa gtt gag att gac tat gcc gtc act cgt gcg gcg    48
Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
 1               5                   10                  15

gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att    96
Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
            20                  25                  30

tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat    144
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
          35                  40                  45

ttt gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa    192
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
        50                  55                  60

ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta    240
Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
65                  70                  75                  80
```

135

```
cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc   288
Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
                85                  90                  95

act gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca   336
Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
                100                 105                 110

gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca   384
Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
                115                 120                 125

atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc   432
Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
        130                 135                 140

ggt aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa   480
Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
145                 150                 155                 160

gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc   528
Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
                165                 170                 175

gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat   576
Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
                180                 185                 190

ttt tca aat cgt tta gca tcg taaggggtag aaaatggctt taccacgcaa      627
Phe Ser Asn Arg Leu Ala Ser
                195

acttaaattg atgaatttaa tcatcgacgg taacaaatat ctcggcgaag tcacggaagt 687 ·

gactcaacca aaattagcaa tgaaaatcga agaatttcgc gcgggcggta tgattggttc 747

ggtggatgtc aatctcgggc ttgaaaagct cgaagcggaa tttaaagccg gtggctacat 807

ggtcgaatta attaaaaaat tcggcgggtc aatcaacggc attccattgc gttttcttgg 867

ctcatatcag cgtgatgaca cagaagaagt cacatctgtt gagcttgtga tgcaaggtcg 927

atttactgaa attgacagcg gaaacagcaa agtgggcgat gacactgaac aaacattcaa 987

agtgccttta acgtattaca aaatcattgt tga                              1020


<210> 67
<211> 199
<212> PRT
<213> Pasteurella multocida

<400> 67
Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
  1                 5                   10                  15

Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
                20                  25                  30

Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
            35                  40                  45
```

136

```
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
    50                  55                  60

Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
65                  70                  75                  80

Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
                85                  90                  95

Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
                100                 105                 110

Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
        115                 120                 125

Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
    130                 135                 140

Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
145                 150                 155                 160

Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
                165                 170                 175

Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
                180                 185                 190

Phe Ser Asn Arg Leu Ala Ser
        195
```

```
<210> 68
<211> 2584
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1042)..(2286)

<220>
<223> xylA

<400> 68
gtcgaccagc ttagattttg cgacggggtt aatttcttct atcgtttcaa tcattgcgtt 60

taccattatt ttatggaatc tctctggacc gatgaccatt gccaatattg aaattcctca 120

cgcgatggtc tttttggtct ttatttacgt gctgtttagc agtattgtgg catttaaaat 180

cggtcgcccg ttaattcagc tcaattttgc caatgaacgc ttaaacgcca actaccgtta 240

ttcacttatc cgtctgaaag aatatgctga aagcattgct ttttatcgtg gtgaaaaaat 300

ggaaaaacgt ctattgacca cacaatttaa tcaggtgatt gataacgttt ggcaagtaat 360

ctaccgcacc ttgaaattat ccggttttaa cttaatcatt acgcagattt cggtggtttt 420

tccgctggtg attcaagtga cacgttattt tcgtcgacaa taggtgcata tgagggtgtt 480

agaatagcga tactttctgt tggaaaagta aactctttaa tataaataga aatcgcttga 540
```

137

atgattctcg ggcaaaaaat aatgtactca tttgcgatct catactgata atggcgaagt 600

aaatatcttc ttacaatatt atggtaatta tcaggtaata ccgtatagcc atagattcca 660

gttctatttt gttttgctaa ataattgatg agcatttgag gcgcaggtaa atccatatct 720

gcaacagaca ttgaaatcat atccttgccg tatttacgag taattgccca tttagcacta 780

tgacaatctg atctatcagt aaaaacatca aacaaattat ccgtcataca tgttctccaa 840

tattggattt atataaactt tagaacttga ggtagattgt tggaattgtt aaatctggta 900

tttctattac gttttttctt ttttgtgata taagccacaa taaccaataa tcttaattgt 960

taagtgaaat aacgtaattg atcctcccat tgttttacta aattatgtct ctgaaactta 1020

tttgttcagg agaaatcatt t atg tcc act tac ttc gac aaa att gaa aaa   1071
                         Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys
                          1   5   10

gta aat tat gaa ggt gta act tca tct aat ccg ttt gca tat aag cat   1119
Val Asn Tyr Glu Gly Val Thr Ser Ser Asn Pro Phe Ala Tyr Lys His
                  15   20   25

tat gat gct aat caa gtt att tta ggt aag acg atg gct gaa cac tta   1167
Tyr Asp Ala Asn Gln Val Ile Leu Gly Lys Thr Met Ala Glu His Leu
              30   35   40

cgt tta gcc gtc tgt tat tgg cac act ttc tgt tgg aca ggg aat gat   1215
Arg Leu Ala Val Cys Tyr Trp His Thr Phe Cys Trp Thr Gly Asn Asp
          45   50   55

atg ttc ggt gtc ggt tct ttc gat cgt tgt tgg cag aag gcg agt gat   1263
Met Phe Gly Val Gly Ser Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp
      60   65   70

tca tta gca ggt gca aaa caa aaa gca gat atc gct ttt gaa ttt ttc   1311
Ser Leu Ala Gly Ala Lys Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe
  75   80   85   90

agt aaa tta ggc ata cct tat tat tgt ttt cat gat gtt gat gtt gcg   1359
Ser Lys Leu Gly Ile Pro Tyr Tyr Cys Phe His Asp Val Asp Val Ala
                  95   100   105

cca gaa ggt cat tca ttt aaa gaa tat ttg tcg aac ttt aat aca atg   1407
Pro Glu Gly His Ser Phe Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met
              110   115   120

atc gat gtt tta gcg cag aaa caa gaa gaa aca ggc gtc aaa ttg ttg   1455
Ile Asp Val Leu Ala Gln Lys Gln Glu Glu Thr Gly Val Lys Leu Leu
          125   130   135

tgg ggg act gca aat tgt ttt aca cac cct cgt tat atg tct ggt gct   1503
Trp Gly Thr Ala Asn Cys Phe Thr His Pro Arg Tyr Met Ser Gly Ala
      140   145   150

gca aca aat ccg aat cca gaa att ttt gct tgg gct gct gca caa gta   1551
Ala Thr Asn Pro Asn Pro Glu Ile Phe Ala Trp Ala Ala Ala Gln Val
155   160   165   170

ttt act gcc atg ggg gca act cag cgt tta ggt ggt gaa aat tat gtt   1599
Phe Thr Ala Met Gly Ala Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val

138

```
ttg tgg gga gga cgt gaa gga tat gaa acg tta tta aat acc aat tta    1647
Leu Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu
        190             195                 200

aaa cag gag cga gag caa att gga cgt ttc atg caa atg gtg gtt gag    1695
Lys Gln Glu Arg Glu Gln Ile Gly Arg Phe Met Gln Met Val Val Glu
        205             210                 215

cat aaa tat aaa atc ggt ttt aac ggg act ttg ctg att gaa cca aag    1743
His Lys Tyr Lys Ile Gly Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys
    220             225                 230

cca caa gag cca acg aaa cat caa tat gac tat gat gtg gcg acc gtt    1791
Pro Gln Glu Pro Thr Lys His Gln Tyr Asp Tyr Asp Val Ala Thr Val
235             240             245                 250

tat ggc ttt tta aag cag ttt ggt tta gaa aaa gaa att aaa gtg aat    1839
Tyr Gly Phe Leu Lys Gln Phe Gly Leu Glu Lys Glu Ile Lys Val Asn
                255             260                 265

att gaa gct aat cac gca aca tta gct gga cac act ttc cag cat gaa    1887
Ile Glu Ala Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu
                270             275                 280

gtc gcc atg gct aca gcg tta gat att ttt ggt tct att gat gca aat    1935
Val Ala Met Ala Thr Ala Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn
            285             290                 295

cgt ggt gat cca caa tta ggt tgg gat acc gat caa ttc cct aat agc    1983
Arg Gly Asp Pro Gln Leu Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser
        300             305             310

gta gaa gaa aat act ttg gtc ata tat gaa att ctc aaa gca ggg ggc    2031
Val Glu Glu Asn Thr Leu Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly
315             320             325                 330

ttt aca acc ggt ggt ttt aat ttt gat gct aaa atc cgt cgg cag agt    2079
Phe Thr Thr Gly Gly Phe Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser
                335             340             345

acg gat cct tac gat tta ttt cat gga cat att ggc gcg att gat gta    2127
Thr Asp Pro Tyr Asp Leu Phe His Gly His Ile Gly Ala Ile Asp Val
                350             355                 360

ctt gcc tta tca cta aaa tgt gcg gcg aaa atg ctt gaa gag caa gct    2175
Leu Ala Leu Ser Leu Lys Cys Ala Ala Lys Met Leu Glu Glu Gln Ala
        365             370                 375

tta caa aaa gtc gtc aat caa cgt tat gct ggt tgg aca tca tca ctt    2223
Leu Gln Lys Val Val Asn Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu
        380             385                 390

ggt caa ctt gtt caa atc cgg tcc tac cac gcg tgt ctg caa tac aga    2271
Gly Gln Leu Val Gln Ile Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg
395             400             405                 410

cta aca aaa gtg ctt taaaacgttc cggcttacgc cagacatcta gacgattgaa    2326
Leu Thr Lys Val Leu
            415
```

139

```
taatttcaat attgtctccg cacgtaattc aaaggctttg tgtatgtgcg aatgatattc 2386

acaacaaagt tctgcaaaat cttgaattgc gtgaggtaat ttaaagcgct gacataagcg 2446

tcttgtcggc atgacaccag cttttcatg tccataatga tgtggcaata tttcttttgg 2506

tgttaaggct tttcctaaat catgacaaat tgcagcaaaa cgtaccgcac ttttgtcact 2566

gtccgtgttt tctgtcga                                              2584


<210> 69
<211> 415
<212> PRT
<213> Pasteurella multocida

<400> 69
Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys Val Asn Tyr Glu Gly Val
  1               5                  10                  15

Thr Ser Ser Asn Pro Phe Ala Tyr Lys His Tyr Asp Ala Asn Gln Val
               20                  25                  30

Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Ala Val Cys Tyr
           35                  40                  45

Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser
       50                  55                  60

Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp Ser Leu Ala Gly Ala Lys
 65                  70                  75                  80

Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe Ser Lys Leu Gly Ile Pro
               85                  90                  95

Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe
              100                 105                 110

Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln
              115                 120                 125

Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys
           130                 135                 140

Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
145                 150                 155                 160

Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala
                  165                 170                 175

Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
              180                 185                 190

Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln
              195                 200                 205

Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly
    210                 215                 220

Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys
225                 230                 235                 240
```

140

```
His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln
            245             250             255

Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala
            260             265             270

Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala
            275             280             285

Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu
            290             295             300

Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu
305             310             315             320

Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe
            325             330             335

Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu
            340             345             350

Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys
            355             360             365

Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn
            370             375             380

Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile
385             390             395             400

Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu
            405             410             415


<210> 70
<211> 3501
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (298)..(1905)

<220>
<223> yabk

<400> 70
gaattcgagg aaggggggcgt attacaaatt gaaacggctg cacgtgtagc acaacatgat 60

aatgcctgtg cggatcattt ccttgccttt ttacttcatc cagaagcaca agggcattta 120

gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180

cttagagcca cccaaatgaa cacgaaagtg ctcgatacct caaaagtgaa tgccgaacaa 240

gtcaaaaaat ggattgctgt ttggcaaacg accctaaccc aataattgtt tgtcttg    297

atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt  345
Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu
 1               5              10              15

ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc  393
```

141

```
Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala
        20              25              30

tta ggg gcg gtt ttt tcg ctc cct ttt gcg cgc agt tgg aca gcg ttg    441
Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu
        35              40              45

ttg agt gat cag tat tta caa cac gtg atc atc ttt agc ttt tgg caa    489
Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln
        50              55              60

gcc ttt ctg tcg gcg gta ctt gcg gtc ctc ttt ggt ggc att gta gca    537
Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala
65              70              75              80

cga gcc ttt ttt tat caa ccg ttt gtg ggc aag aaa ctg atc ctc aaa    585
Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys
                85              90              95

tta ttt tca ctg act ttt gtg tta cct gcc tta gtg gcg att ttt ggt    633
Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly
        100             105             110

tta tta ggc gtg tat ggc gct tct ggc tgg tta gcg atg tta agc cag    681
Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln
        115             120             125

ttt ttc gct tgg gat tgg act cct aat att tac ggc tta aca ggt att    729
Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile
        130             135             140

tta ctg gcg cat ctt ttt ttt aat gtc cca tta gct tgt cgc ctg ttt    777
Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe
145             150             155             160

tta caa ggt ttg caa gca att ccg gtg caa caa cgt cag ctc gcg gca    825
Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala
        165             170             175

caa ctc aat tta cgt ggt tgg cat ttt ata cgt ctg att gag tgg ccc    873
Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro
        180             185             190

tat tta cgc cag caa ttg tta cct gca ttt act ttg att ttc atg ctg    921
Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu
        195             200             205

tgt ttt acc agt ttt gcg att gtg ctc act tta ggt ggc gga ccg aaa    969
Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys
        210             215             220

tat acc acg ttg gaa gtg gct atc tat caa gcg att tta ttt gag ttt    1017
Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe
225             230             235             240

gat gta ccg aaa gcc ggc tta ttt gcg tta tta caa ttt gtt ttt tgt    1065
Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys
        245             250             255

ttt ctg tta ttc acg ctg agt agc ttt ttt tct cca gcc ccc gcc acg    1113
Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr
        260             265             270
```

142

```
aca tta cac agt caa cct act tgg ttt gcg ccc caa tcg tat tgg gtt    1161
Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val
        275                 280                 285

aaa tta tgg caa cgt atg atc att gtg tgt gcg aca gta ttt atc tta    1209
Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu
        290                 295                 300

tta ccg cta ctc aat acg cta gtt tct gct ttg ctt tcg tct cag ttt    1257
Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe
305                 310                 315                 320

ttt acc ttg tgg tta caa cct caa tta tgg aaa gca tta ggt tac tcg    1305
Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser
                325                 330                 335

ctc acc atc gcc ccc act tct gca ttg ctc gct tta gta ctg tct ttt    1353
Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe
                340                 345                 350

gcc tta tta ttg ctt gcc aga gaa tta cat tgg cga cat tat cgc agc    1401
Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser
        355                 360                 365

tta tcc cat gtg att tta aat atc ggt gcg acc att tta gcc att cca    1449
Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro
        370                 375                 380

acg tta gtg tta gct att ggt tta ttc att tta tta cgt gag atc gat    1497
Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp
385                 390                 395                 400

ttt tct cca tac cat ctt ttt ggg gtt gtg gta tgc tgt aac gcg tta    1545
Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu
                405                 410                 415

gct gct atg cct ttt gtg ttg cgt att ttg gct tta ccg atg cat aac    1593
Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn
                420                 425                 430

aat atg att tat tat gaa aaa tta tgc caa tca ctt aac ctg cgt ggt    1641
Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly
                435                 440                 445

tgg caa cgt ttt cga ttg att gaa tgg cac aag ctt cgt gcg cca atg    1689
Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met
        450                 455                 460

aaa tac gcc ttt gca ctg gct tgt gcg tta tca tta ggc gat ttc acc    1737
Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr
465                 470                 475                 480

gca atc gcg tta ttt ggt cag gct gac ttc aca tcg tta ccg cat ttg    1785
Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu
                485                 490                 495

ttg tat caa caa ttg ggg cat tat cgt agt cag gaa gcg gca gta aca    1833
Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr
        500                 505                 510

gcg ttt att tta ttg gtt ttt tgt ttg agt gtt ttt atg att att gaa    1881
Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu
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143

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cga cat cag gaa ccg cgt gat gat taatttaaac ggtgttcagt tttcctataa  1935
Arg His Gln Glu Pro Arg Asp Asp
   530                535

taccttтact tttgagctgg atttgcagat tcctgctcaa caaaaagttg ctattattgg  1995

cgccagtggc gcagggaaga gtaccttatt aaatttgatt gcgggttttg cattgccaca  2055

gcaaggggaa atttggttga atggtgaaaa tcatagccaa actcaacctt atgaacgtcc  2115

ggtatctatt ttgtttcaag aaaacaactt gtttacgcat ttgactgtgg cagagaatat  2175

ggcattaggg ctgaaaccaa gcctaaaact gaccgcactt gaacaacaac gcgtacaaca  2235

agtggcaagt gcagtgggtt tgcagggttt tcttaatcaa ttacccaccc agttatcggg  2295

tgggcaaaaa cagcgtgtgg cgttggcgcg ttgtttatta cgcgataagc caattttgtt  2355

attggatgaa ccttttтctg ccttagatcc cgatttacgg gcagaaatgt tgcatttatt  2415

gttacagttg tgtgatgaaa aaaaattaac actcctgatc gtgacacatc aagtgaacga  2475

attacagcag aaaatggatc gtatgattcg ttttgaacat ggtaggatga gtgagtccac  2535

cattttgaag gataatttta acgaaaaaca gaccgcactt taggcggctt attaattaga  2595

taaggaaaga gaaaaatatg acaacggcaa cggcatttga gattcgtaca cttactcctc  2655

acccgacctt agaatattgg tctgtgtgta aaattgaagc cctgtttgag accccttttt  2715

tagatttggt ttatcgggct gcgcaagtgc accgagaaaa ctttaatcct aaagccattc  2775

aattatccac tttaatgtcg attaaaacgg ggggatgtcc agaggattgt ggctactgtc  2835

cgcagtcagc acgttatcat actggagtag aaaagcagca attactcgat gtggaagaaa  2895

ttgttgaaaa agccaaaatt gccaaagcac gtggtgcagg gcgcttttgt atggggggctg  2955

catggcgtgg accgaaaccg aaagacattg aaaaagttac cgcaatcatt aaagcggtga  3015

aagaactggg cttagaaacc tgtggtacct ttggtttatt gcaagatggg atggcagaag  3075

atttaaaaga agcgggtttg gattattata accataatct cgatacagcc ccagaacact  3135

acggtaatgt gattggtacc cgtcaatttg atgatcgtat taatacgtta ggtaaagtgc  3195

gtaaagctgg cttaaaagtg tgctgtggcg ggattattgg catgaatgaa acccgtaaag  3255

aaagagcagg attaattgct agcttagcta atttagaccc gcaacccgaa tcggtgccga  3315

ttaatcaatt agtgaaagtg gaaggtaccc ctttagccga tgcggcagaa ttagactgga  3375

cagaatttgt gcgcactatt gcggtggcgc gtattaccat gccgaaaagc tatgtacgtt  3435

tatcagcagg gcgtcaaggc atgtcggaag aaatgcaagc catgtgcttt atggctggcg  3495

cgaatt                                                           3501
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<210> 71
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<211> 536
<212> PRT
<213> Pasteurella multocida

<400> 71
Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu
 1   5   10   15

Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala
            20   25   30

Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu
        35   40   45

Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln
    50   55   60

Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala
65   70   75   80

Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys
                85   90   95

Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly
                100   105   110

Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln
            115   120   125

Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile
    130   135   140

Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe
145   150   155   160

Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala
                165   170   175

Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro
                180   185   190

Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu
            195   200   205

Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys
    210   215   220

Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe
225   230   235   240

Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys
            245   250   255

Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr
            260   265   270

Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val
        275   280   285

Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu
    290   295   300

145

```
Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe
305             310             315                 320

Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser
            325             330             335

Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe
            340             345             350

Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser
        355             360             365

Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro
        370             375             380

Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp
385             390             395                 400

Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu
            405             410             415

Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn
            420             425             430

Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly
            435             440             445

Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met
        450             455             460

Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr
465             470             475                 480

Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu
            485             490             495

Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr
            500             505             510

Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu
            515             520             525

Arg His Gln Glu Pro Arg Asp Asp
    530             535


<210> 72
<211> 3182
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1544)..(2809)

<220>
<223> ygiK

<400> 72
aactactaag gagttatgta tgaatattag aaaatcatta ctattaatat ccctagcaag  60

cttcatgtca ctttcagttt cagctgcaga aattaatttg aaatttgaaa gttcgaattt  120
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146

```
tgcaggagaa aaagtttatg aaatccaaaa agaatggact gacaatattg aaaaagcttc  180

caatgggaga ataagtatag agttattacc tctcgactca gtcttaaaat ctagtgacat  240

gctttctggt gttcgaaata aaattattga tggagcggtt gcaacagcgg caatgtatgc  300

aggcactgac cctggattcg gattaattgg tgatactatt tctgcttgga accatgacga  360

agatatttta aatttttact ataatggagg tggttttgaa gttgttgata atattttcca  420

acaatatggt gccaaactca ttggtgtatc anttacggga gcagaatcat taccatcgaa  480

agtaaaaata gctaatactg aagattttaa aggtataaaa attcgggctc cctctggtcc  540

tatccaaaaa ttgtttgcaa gattaggagc cgctcctgtt ggtcttcctg gttcagaaat  600

ctatactagt ttagaaaaag gtattattga tgctgccgat ttctcaacgt ttgcaaataa  660

tcaagcacaa ggagtccatg atattgcaaa atatccaatc tatccgggaa ttcattcttc  720

accagccgtt catatgatta tgaatcataa aacttggagt agcttaactc catcggatca  780

agcattctta attgcttact ttaaagggat ggctctcgat actctgactc gtgctcatta  840

tgaagataaa ctagcatata aagaagcact tgagaaagga gtacaaccag tttcttggaa  900

tcaacaagaa attacaaaag ttcgttctat cgctaagaa atttggcaag agatagctca  960

acaatctgaa ataggtaatc aagtattatc aagtattaat gaaattccta gaatctcaag  1020

gaatgctgca ataatcgtca agatggataa gacgatatcg tcttatccat taaggagtaa  1080

aacatgctta tttctaaata tttattatgg ctctgtaata agctagatca aatattcatt  1140

aaagtaggtt attacgtttc ttatattttt ctattagttg ttatcattgg ttttacgagg  1200

ttgttgctcg gtatttattc tctagcccaa cactttgggt tcatgaagta acaacatttt  1260

taataagtct atcattactt tatggtggag tagcttgtta cgccagtaat aaacatattg  1320

ccatgacatt tattagacaa aaattaccta ataagatcaa atggttacta gaactcttag  1380

ttgaaatact tattttttatc ttctttattt tgcttagtta cggagcatac ttatcagcta  1440

gagaagcatt atttactcca tcaggaaaat tcaaaatgca aacttctgga agtgtattag  1500

acatgccatt tccagcaatt gaaaaaagtt tcttctttat ttc atg cct cat cat      1555
                                              Met Pro His His
                                               1

tgt tgt tct ttc agt act aca tat att ccg tca cat cta tac aaa ata      1603
Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His Leu Tyr Lys Ile
 5                  10                  15                  20

tca gga gga att atc atg ata agt gca ttt ggg ata ggt att gga act      1651
Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile Gly Ile Gly Thr
                25                  30                  35

ctt att atc ttt tta atg atg att tcc ctt tta ttt att gga atg cca      1699
Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe Ile Gly Met Pro
            40                  45                  50
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147

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tta ggt ttt ctc act ggg tta atc gct tta gtt att tca tat ctt tgg    1747
Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile Ser Tyr Leu Trp
        55                      60                  65

ttt gat act acc gca ata atg caa atg ata gct tca cgt gtc act gat    1795
Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser Arg Val Thr Asp
        70                      75                  80

ttc aca tca tct tac act ttt gta gct gtg cct atg ttt gtt ctt atg    1843
Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met Phe Val Leu Met
85                      90                  95                  100

gca aca tta ctt gat aag act gga att gct aga gat ctc tac aac gca    1891
Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp Leu Tyr Asn Ala
                105                     110                 115

atg cga gtc att ggc ggt cga tta cga ggt gga att gca att caa tcg    1939
Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile Ala Ile Gln Ser
                120                     125                 130

atg ttt gtt gca gtt cta ctt gct acg atg tca ggt att atc ggt gga    1987
Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly Ile Ile Gly Gly
                135                     140                 145

gaa act gtt tta tta ggc atg ttg gca tta cca caa atg tta cgc tta    2035
Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln Met Leu Arg Leu
        150                     155                 160

ggc tat aat aaa aac tta gct ata gga act gtt gta gca gga gga gca    2083
Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val Ala Gly Gly Ala
165                     170                 175                 180

ttg ggt aca atg gtt cct cca agt atc gtg ttg att att tac gga atg    2131
Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile Ile Tyr Gly Met
                185                     190                 195

acc gca aat gtt tct att gga gaa cta ttt ctt gca gca att cca gcc    2179
Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala Ala Ile Pro Ala
                200                     205                 210

tcc tta cta ctt tct aca ttc tat att tta tat att cta gta ctt tgc    2227
Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile Leu Val Leu Cys
                215                     220                 225

tac ttc aaa cct agc tat ggc cct gca atg cct agc tca gaa aat cat    2275
Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser Ser Glu Asn His
        230                     235                 240

aca tta acg aaa gaa gat att aaa aaa att att cat gat att gca att    2323
Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His Asp Ile Ala Ile
245                     250                 255                 260

cca gta gct atc gcc aca tgg att tta gga agt att tat ggc ggg ata    2371
Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile Tyr Gly Gly Ile
                265                     270                 275

gca tca atc act gaa tct gcc tgt gtt ggt gta gtt ggg gta ata tta    2419
Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val Gly Val Ile Leu
                280                     285                 290

gca gca ttc tat cga aaa gaa tta aat ttc aaa ata gta caa gaa tca    2467
Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile Val Gln Glu Ser
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148

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cta aaa cat aca atc aat act gtt ggt atg ata atc tgg gtc ggc att   2515
Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile Trp Val Gly Ile
    310                 315                 320

ggc gca aca atg att ata ggt att tat aat cta atg ggt ggg gac cga   2563
Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met Gly Gly Asp Arg
325                 330                 335                 340

ttt ata gct aac tta ttc gct agc tta gat gcc tct cca att tat act   2611
Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser Pro Ile Tyr Thr
                345                 350                 355

atc att att atg atg gtt att tta tta ata ctt ggt atg ttc tta gat   2659
Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly Met Phe Leu Asp
            360                 365                 370

tgg att ggt gtt gcc atg ttg act ttc ctc aag aca agt aaa gcg aca   2707
Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr Ser Lys Ala Thr
            375                 380                 385

atc aat ttg tgt ttt gac ata gtc agg tac agt att tgg cgt ggt ccc   2755
Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile Trp Arg Gly Pro
    390                 395                 400

tcc ttc cac agt acc aat gtt cat cgt ggt acc ttt gtc ggg cgc ggt   2803
Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe Val Gly Arg Gly
405                 410                 415                 420

act ttt tagtaaatct tgcgcgatac gaataaacgc attgatggca tttgctccgt   2859
Thr Phe

tttgtggatc gactgccgca tgagcagatt tgccaaaaaa ttcaattaca tacttcccaa 2919

tcccttttct ttcgttaacg tttccactta gattgcccag aagccgatct gtctgaatgg 2979

gaacaagtgt tataccaaga agcgaatcca acaggtgaag tggtgatcgg tatggtgggt 3039

aaatacactg aattaccgga tgcctacaaa tcggttaatg aagccttgaa acacgcaggc 3099

ttaaaaaacc gtcttagcgt gcaaatcaaa tatattgatt cacaagatgt ggaaaccaaa 3159

ggcacagaag tgttagaagg cgt                                        3182
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<210> 73
<211> 422
<212> PRT
<213> Pasteurella multocida

<400> 73
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Met Pro His His Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His
 1               5                  10                  15

Leu Tyr Lys Ile Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile
            20                  25                  30

Gly Ile Gly Thr Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe
        35                  40                  45

Ile Gly Met Pro Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile
```

Ser Tyr Leu Trp Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser
65   70   75   80

Arg Val Thr Asp Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met
              85   90   95

Phe Val Leu Met Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp
              100   105   110

Leu Tyr Asn Ala Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile
              115   120   125

Ala Ile Gln Ser Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly
              130   135   140

Ile Ile Gly Gly Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln
145   150   155   160

Met Leu Arg Leu Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val
              165   170   175

Ala Gly Gly Ala Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile
              180   185   190

Ile Tyr Gly Met Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala
              195   200   205

Ala Ile Pro Ala Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile
              210   215   220

Leu Val Leu Cys Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser
225   230   235   240

Ser Glu Asn His Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His
              245   250   255

Asp Ile Ala Ile Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile
              260   265   270

Tyr Gly Gly Ile Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val
              275   280   285

Gly Val Ile Leu Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile
              290   295   300

Val Gln Glu Ser Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile
305   310   315   320

Trp Val Gly Ile Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met
              325   330   335

Gly Gly Asp Arg Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser
              340   345   350

Pro Ile Tyr Thr Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly
              355   360   365

Met Phe Leu Asp Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr
370   375   380

```
Ser Lys Ala Thr Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile
385                 390                 395                 400

Trp Arg Gly Pro Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe
                405                 410                 415

Val Gly Arg Gly Thr Phe
                420


<210> 74
<211> 2787
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (463)..(936)

<220>
<223> yhcJ

<400> 74
gttaacacac catgattaat gatgccggtt gaagccactg caacgtaatc gaattgtccg 60

gcatacaaag caagaatgtt ggccagtgtg tcatgcatcg cattggcagc atcagcttgt 120

ggcgttgcaa tctgttggcg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180

tttgttccac caatatctaa tgctaaacag cgcataggct ctccttctgt gatgacttat 240

tttgccgatt tgacggcatc ggcaaaccag cttacgatat gttcgaggcg agtcagcgca 300

gatcctacgg tgacagagta agcaccaatc tcaattgcgg ttttcgccaa ttctggggtg 360

ttatagcgcc cttctgccat cactcggcag ccagcagcat tcaaatcttt gactaactga 420

taatccggtt cagctggaat ttcaccgcca gtataaccag ac atg gtg cta cca    474
                                                 Met Val Leu Pro
                                                  1

ata att tct acc cct aag ttg tgg caa tac atc cct tct tca aaa tta   522
Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro Ser Ser Lys Leu
  5                  10                  15                  20

gaa caa tcc gcc atg gct aaa caa cct aat tct ttg att cgt tta ata   570
Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu Ile Arg Leu Ile
                 25                  30                  35

atg gct tca cgt gta gtt gga cgg acg cga tcg gta cca tca aaa gca   618
Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val Pro Ser Lys Ala
                 40                  45                  50

ata ata tcg gcg cct gct gcg gct aac tct tca atg tct tgt aaa aat   666
Ile Ile Ser Ala Pro Ala Ala Ala Asn Ser Ser Met Ser Cys Lys Asn
         55                  60                  65

ggg cta ata cga acg gga ctg tca ggt aaa tcg cgt tta acg ata cca   714
Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg Leu Thr Ile Pro
     70                  75                  80

ata atc ggt aca ttg acg acg tta cgc gtg gct ttt aaa ttt tcg atc   762
```

151

```
Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe Lys Phe Ser Ile
 85                  90              95                  100

cct tca ata cgt aac ccg gca gca cca ccg ata acg gat gct tgc gcc   810
Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr Asp Ala Cys Ala
                105                 110                 115

atg gcg gca aca att tct ggc gag tcc att ggc cca tta tct acg ggc   858
Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro Leu Ser Thr Gly
                120                 125                 130

tgg caa gat gcg att aag cca tat tta att tgt tct aaa act tgc gga   906
Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser Lys Thr Cys Gly
            135                 140                 145

tgt gat agt ttt gac ata tta act cca gtc taaatttatc aaaagaagat     956
Cys Asp Ser Phe Asp Ile Leu Thr Pro Val
        150                 155

tgactccaat ttgcataggt taatcttaga attaaaaaat aacaaccaaa ataataaaaa 1016

tttgagatct ttgtcgcata tttattcata gggaatagac agcttaattt tagttatgat 1076

ttgtcaatcc ttgctatttt ttgtgtttgc tggtttgcga tacactgttc taatattgct 1136

ttgagcactt gataaccttg ctcattaaaa tgtaatccgt cggtacaaag gcgtaaatcc 1196

agttcaccgt tagaatcaca aaagtatttt tgtgtttcaa cgtaagtcac gtctgacgga 1256

caatgttgtt ttaaataggt attgagcctg tgaatttgtg cgttagtgac cgtattaatc 1316

tgattgaccg gtgtggcttc taataaaaag tagtgggacg taggagaaat ggtgtgtagg 1376

tgagtcagaa tgtcatttaa ctatcgcatg acttgcgccg gtgaatacgt ttcttcctta 1436

caaatatcat tgacgcctaa aaaaagaaaa acagattgtc caagttgttg aatccgttta 1496

ggtttaacga taacatccaa atattgtcgc gtactgacgc cagaaagtcc taaattggcg 1556

acggtttgtc ccgctaattg aggtgtgcct gctacctgtt cgtcccacat gtcaaaaagt 1616

gaatgaccaa ttaagctgat attggcaggt ttggaaaatt ccgccatttt gctctgatag 1676

cgttgataaa tatcctgatc acttagcatg tgtggacctc tattttgaaa taaaacgcta 1736

agtattatat aaaacctgat atgccggtaa acagtaaact tatcttccgt aggggtaaat 1796

attcaatttt gtgacgaacc tatcatttat gaaataaaac ttcattttct atataaaaaa 1856

tagttttttc actttagaat gccaaacgtg tgaaatttat ttcatcatca ttttaacgta 1916

atcccaacgt aaccaataga ggagaactca taatgaaatt taaaaaacta ctacttgcat 1976

ctttatgttt aggtgtttca gcttctgtat ttgcagcaga ttacgatctt aaattcggta 2036

tggttgcggg tccaagctca aacgaatata aagcagtaga attctttgcg aaagaagtga 2096

aagaaaaatc caatggcaaa attgatgtgg ctattttccc tagctcacag ttaggtgatg 2156

accgtgtgat gattaaacaa ttaaaagacg gtgcattaga ctttacgtta ggtgaatcag 2216

cacgtttcca aatttacttc ccagaagcag aagtatttgc gttgccttat atgattccta 2276
```

152

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attttgaaac ctctaaaaaa gcgttgctcg acacaaaatt tggtcaaggt ttattgaaaa 2336

aaattgataa agagttaaac gtacaagtgt tatctgtggc gtataacggt acacgtcaaa 2396

caacttctaa ccgtgcaatc aacagcattg aagacatgaa agggttaaaa ttacgtgtac 2456

ctaacgcggc aaccaacctt gcttatgcaa aatacgtggg tgcagcgcca acaccaatgg 2516

cattctctga agtttacctt gcgcttcaaa caaactctgt ggatggtcaa gaaaacccat 2576

taccgacaat ccaagcacaa aaattctatg aagtacaaaa atacttagcg ttaactaacc 2636

acatcttaaa tgaccaactt tacttaatca gtaacgatac gttggcagat ttaccagaag 2696

atttacaaaa agtggttaaa gatgcagcag cgaaagccgc tgaatatcac actaaactct 2756

tcgttgacgg tgagaacagc ttagttgaat t                           2787
```

<210> 75
<211> 158
<212> PRT
<213> Pasteurella multocida

<400> 75

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Met Val Leu Pro Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro
 1               5                   10                  15

Ser Ser Lys Leu Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu
            20                  25                  30

Ile Arg Leu Ile Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val
        35                  40                  45

Pro Ser Lys Ala Ile Ile Ser Ala Pro Ala Ala Ala Asn Ser Ser Met
    50                  55                  60

Ser Cys Lys Asn Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg
65                  70                  75                  80

Leu Thr Ile Pro Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe
                85                  90                  95

Lys Phe Ser Ile Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr
            100                 105                 110

Asp Ala Cys Ala Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro
            115                 120                 125

Leu Ser Thr Gly Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser
    130                 135                 140

Lys Thr Cys Gly Cys Asp Ser Phe Asp Ile Leu Thr Pro Val
145                 150                 155
```

<210> 76
<211> 2787
<212> DNA
<213> Pasteurella multocida

<220>

153
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<221> CDS
<222> (1949)..(2785)

<220>
<223> yiaO

<400> 76
gttaacacac catgattaat gatgccggtt gaagccactg caacgtaatc gaattgtccg 60

gcatacaaag caagaatgtt ggccagtgtg tcatgcatcg cattggcagc atcagcttgt 120

ggcgttgcaa tctgttggcg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180

tttgttccac caatatctaa tgctaaacag cgcataggct ctccttctgt gatgacttat 240

tttgccgatt tgacggcatc ggcaaaccag cttacgatat gttcgaggcg agtcagcgca 300

gatcctacgg tgacagagta agcaccaatc tcaattgcgg ttttcgccaa ttctggggtg 360

ttatagcgcc cttctgccat cactcggcag ccagcagcat tcaaatcttt gactaactga 420

taatccggtt cagctggaat ttcaccgcca gtataaccag acatggtgct accaataatt 480

tctacccccta agttgtggca atacatccct tcttcaaaat tagaacaatc cgccatggct 540

aaacaaccta attctttgat tcgtttaata atggcttcac gtgtagttgg acggacgcga 600

tcggtaccat caaaagcaat aatatcggcg cctgctgcgg ctaactcttc aatgtcttgt 660

aaaaatgggc taatacgaac gggactgtca ggtaaatcgc gtttaacgat accaataatc 720

ggtacattga cgacgttacg cgtggctttt aaattttcga tcccttcaat acgtaacccg 780

gcagcaccac cgataacgga tgcttgcgcc atggcggcaa caatttctgg cgagtccatt 840

ggcccattat ctacgggctg gcaagatgcg attaagccat atttaatttg ttctaaaact 900

tgcggatgtg atagttttga catattaact ccagtctaaa tttatcaaaa gaagattgac 960

tccaatttgc ataggttaat cttagaatta aaaaataaca accaaaataa taaaaatttg 1020

agatctttgt cgcatattta ttcataggga atagacagct taattttagt tatgatttgt 1080

caatccttgc tattttttgt gtttgctggt ttgcgataca ctgttctaat attgctttga 1140

gcacttgata accttgctca ttaaaatgta atccgtcggt acaaaggcgt aaatccagtt 1200

caccgttaga atcacaaaag tattttgtg tttcaacgta agtcacgtct gacggacaat 1260

gttgttttaa ataggtattg agcctgtgaa tttgtgcgtt agtgaccgta ttaatctgat 1320

tgaccggtgt ggcttctaat aaaaagtagt gggacgtagg agaaatggtg tgtaggtgag 1380

tcagaatgtc atttaactat cgcatgactt gcgccggtga atacgtttct tccttacaaa 1440

tatcattgac gcctaaaaaa agaaaaacag attgtccaag ttgttgaatc cgtttaggtt 1500

taacgataac atccaaatat tgtcgcgtac tgacgccaga aagtcctaaa ttggcgacgg 1560

tttgtcccgc taattgaggt gtgcctgcta cctgttcgtc ccacatgtca aaaagtgaat 1620

gaccaattaa gctgatattg gcaggtttgg aaaattccgc cattttgctc tgatagcgtt 1680

154

gataaatatc ctgatcactt agcatgtgtg gacctctatt ttgaaataaa acgctaagta 1740

ttatataaaa cctgatatgc cggtaaacag taaacttatc ttccgtaggg gtaaatattc 1800

aattttgtga cgaacctatc atttatgaaa taaaacttca ttttctatat aaaaaatagt 1860

tttttcactt tagaatgcca aacgtgtgaa atttatttca tcatcatttt aacgtaatcc 1920

caacgtaacc aatagaggag aactcata atg aaa ttt aaa aaa cta cta ctt        1972
                                Met Lys Phe Lys Lys Leu Leu Leu
                                 1                   5

gca tct tta tgt tta ggt gtt tca gct tct gta ttt gca gca gat tac        2020
Ala Ser Leu Cys Leu Gly Val Ser Ala Ser Val Phe Ala Ala Asp Tyr
     10              15                  20

gat ctt aaa ttc ggt atg gtt gcg ggt cca agc tca aac gaa tat aaa        2068
Asp Leu Lys Phe Gly Met Val Ala Gly Pro Ser Ser Asn Glu Tyr Lys
 25              30                  35                      40

gca gta gaa ttc ttt gcg aaa gaa gtg aaa gaa aaa tcc aat ggc aaa        2116
Ala Val Glu Phe Phe Ala Lys Glu Val Lys Glu Lys Ser Asn Gly Lys
                 45                  50                  55

att gat gtg gct att ttc cct agc tca cag tta ggt gat gac cgt gtg        2164
Ile Asp Val Ala Ile Phe Pro Ser Ser Gln Leu Gly Asp Asp Arg Val
                 60                  65                  70

atg att aaa caa tta aaa gac ggt gca tta gac ttt acg tta ggt gaa        2212
Met Ile Lys Gln Leu Lys Asp Gly Ala Leu Asp Phe Thr Leu Gly Glu
             75                  80                  85

tca gca cgt ttc caa att tac ttc cca gaa gca gaa gta ttt gcg ttg        2260
Ser Ala Arg Phe Gln Ile Tyr Phe Pro Glu Ala Glu Val Phe Ala Leu
     90                  95                  100

cct tat atg att cct aat ttt gaa acc tct aaa aaa gcg ttg ctc gac        2308
Pro Tyr Met Ile Pro Asn Phe Glu Thr Ser Lys Lys Ala Leu Leu Asp
105                 110                 115                 120

aca aaa ttt ggt caa ggt tta ttg aaa aaa att gat aaa gag tta aac        2356
Thr Lys Phe Gly Gln Gly Leu Leu Lys Lys Ile Asp Lys Glu Leu Asn
                 125                 130                 135

gta caa gtg tta tct gtg gcg tat aac ggt aca cgt caa aca act tct        2404
Val Gln Val Leu Ser Val Ala Tyr Asn Gly Thr Arg Gln Thr Thr Ser
                 140                 145                 150

aac cgt gca atc aac agc att gaa gac atg aaa ggg tta aaa tta cgt        2452
Asn Arg Ala Ile Asn Ser Ile Glu Asp Met Lys Gly Leu Lys Leu Arg
             155                 160                 165

gta cct aac gcg gca acc aac ctt gct tat gca aaa tac gtg ggt gca        2500
Val Pro Asn Ala Ala Thr Asn Leu Ala Tyr Ala Lys Tyr Val Gly Ala
     170                 175                 180

gcg cca aca cca atg gca ttc tct gaa gtt tac ctt gcg ctt caa aca        2548
Ala Pro Thr Pro Met Ala Phe Ser Glu Val Tyr Leu Ala Leu Gln Thr
185                 190                 195                 200

aac tct gtg gat ggt caa gaa aac cca tta ccg aca atc caa gca caa        2596
Asn Ser Val Asp Gly Gln Glu Asn Pro Leu Pro Thr Ile Gln Ala Gln

155

```
aaa ttc tat gaa gta caa aaa tac tta gcg tta act aac cac atc tta     2644
Lys Phe Tyr Glu Val Gln Lys Tyr Leu Ala Leu Thr Asn His Ile Leu
            220                 225                 230

aat gac caa ctt tac tta atc agt aac gat acg ttg gca gat tta cca     2692
Asn Asp Gln Leu Tyr Leu Ile Ser Asn Asp Thr Leu Ala Asp Leu Pro
            235                 240                 245

gaa gat tta caa aaa gtg gtt aaa gat gca gca gcg aaa gcc gct gaa     2740
Glu Asp Leu Gln Lys Val Val Lys Asp Ala Ala Ala Lys Ala Ala Glu
        250                 255                 260

tat cac act aaa ctc ttc gtt gac ggt gag aac agc tta gtt gaa tt      2787
Tyr His Thr Lys Leu Phe Val Asp Gly Glu Asn Ser Leu Val Glu
265                 270                 275
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<210> 77
<211> 279
<212> PRT
<213> Pasteurella multocida

<400> 77
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Met Lys Phe Lys Lys Leu Leu Leu Ala Ser Leu Cys Leu Gly Val Ser
1               5                   10                  15

Ala Ser Val Phe Ala Ala Asp Tyr Asp Leu Lys Phe Gly Met Val Ala
            20                  25                  30

Gly Pro Ser Ser Asn Glu Tyr Lys Ala Val Glu Phe Phe Ala Lys Glu
            35                  40                  45

Val Lys Glu Lys Ser Asn Gly Lys Ile Asp Val Ala Ile Phe Pro Ser
        50                  55                  60

Ser Gln Leu Gly Asp Asp Arg Val Met Ile Lys Gln Leu Lys Asp Gly
65                  70                  75                  80

Ala Leu Asp Phe Thr Leu Gly Glu Ser Ala Arg Phe Gln Ile Tyr Phe
                85                  90                  95

Pro Glu Ala Glu Val Phe Ala Leu Pro Tyr Met Ile Pro Asn Phe Glu
            100                 105                 110

Thr Ser Lys Lys Ala Leu Leu Asp Thr Lys Phe Gly Gln Gly Leu Leu
        115                 120                 125

Lys Lys Ile Asp Lys Glu Leu Asn Val Gln Val Leu Ser Val Ala Tyr
        130                 135                 140

Asn Gly Thr Arg Gln Thr Thr Ser Asn Arg Ala Ile Asn Ser Ile Glu
145                 150                 155                 160

Asp Met Lys Gly Leu Lys Leu Arg Val Pro Asn Ala Ala Thr Asn Leu
                165                 170                 175

Ala Tyr Ala Lys Tyr Val Gly Ala Ala Pro Thr Pro Met Ala Phe Ser
            180                 185                 190

Glu Val Tyr Leu Ala Leu Gln Thr Asn Ser Val Asp Gly Gln Glu Asn
```

156

```
              195                    200                    205
    Pro Leu Pro Thr Ile Gln Ala Gln Lys Phe Tyr Glu Val Gln Lys Tyr
         210                    215                    220
    Leu Ala Leu Thr Asn His Ile Leu Asn Asp Gln Leu Tyr Leu Ile Ser
    225                    230                    235                    240
    Asn Asp Thr Leu Ala Asp Leu Pro Glu Asp Leu Gln Lys Val Val Lys
                        245                    250                    255
    Asp Ala Ala Ala Lys Ala Ala Glu Tyr His Thr Lys Leu Phe Val Asp
                        260                    265                    270
    Gly Glu Asn Ser Leu Val Glu
              275
```

<210> 78
<211> 2590
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (908)..(1294)

<220>
<223> yigF

<400> 78
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ctgcaggctc gattagtggg gcaccgaaag aaaaaaccgt gcaaattatt cacgccgcag  60
aacagcagcc acgcggttat tacacgggga tttttggtct gttcgatggt gagtcgttac 120
aaagtgcggt ggcaattcgt tttattgagc aagtggacga gaaattgatt ttccgcagcg 180
gtggcgggat tacgatctta agcgagctag aagacgagta ccaagaattg atccaaaaag 240
tgtatgtacc agtaggataa gcgatgacat ttcctttatt tgagacgatc gctattgtga 300
acggtgaaat tcagcacctt gccctgcatc aacaacgtta tgcggcaagt ttggcgacct 360
tttacggcga gaaaggagcg aaagtacagg atcttgcgaa aattattcag attccgaccg 420
cacttgaaca cactcaacat gcgccgataa tccgttgtcg gattgattac aatcagcaag 480
actgtgacgt gcattatttt ccctatcaac gcaaaattta ccgcactttt cagcctgtca 540
tttgcgatga aattaactat gatctgaaat atgctgatcg ggcattatta aatcagttat 600
ttgctcagcg tagggattgt gatgagatta tgattatcaa acacggcaag gtgacggatt 660
gcagtattgg taatctggtg tttcgccaag gtgagcaatg gttcacgcca gatagcccgt 720
tattttacgg cacacaacga gcctggttat tacaacaagg caaaattcaa gcccgttcca 780
tcttattgca agagatcgca caatttgaag aaattcggtt aattaatgca ctaaatccgc 840
tgtaaatttt ccttgaacag cgtaaaataa aacaactttt tcagtcagat aaaaggagat 900
aaacgac atg acg aaa gta att cat act gac aat gca cca gcc gcc att     949
```

157

```
             Met Thr Lys Val Ile His Thr Asp Asn Ala Pro Ala Ala Ile
                  1               5                  10

ggt cct tat gta caa gcg gta gat tta ggt aat atg ctg tta acc tct     997
Gly Pro Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser
 15              20                  25                  30

ggg caa att cca gtg aat cca aaa acc ggt gaa gtg cca gcg gat atc    1045
Gly Gln Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile
                 35                  40                  45

gta gca caa gca cgt caa tcg tta gaa aac gtg aaa gcg att gtg gaa    1093
Val Ala Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu
             50                  55                  60

caa gcg gga tta caa gtc gca aat atc gtg aaa acc acg gtg ttt gtg    1141
Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val
             65                  70                  75

aaa gat tta aat gac ttt gca gcg gtc aat gcg gag tat gaa cgt ttc    1189
Lys Asp Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe
         80                  85                  90

ttt aaa gag aac aat cac cct agc ttc cct gct cgt tca tgt gtg gaa    1237
Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu
 95                 100                 105                 110

gtg gca cgt ttg ccg aaa gat gtg ggg att gaa atc gag gca atc gct    1285
Val Ala Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala
                115                 120                 125

gta aaa gcc taatgaatag cttgcattta tcttagtcgt agcaaaacaa            1334
Val Lys Ala

tctctttttca cttgctctct tcaaagcaag ttgataagtg attttattg ggcgttttc  1394

tattgatagc caaaaacgcc ctttactgat agagaataaa ctatgcaaaa tcaagtcatc  1454

gagattctac aataccgttt aaaaccacaa tcaggacaaa cgtttcacca aattatgcgt  1514

gagatcagtg ttccactcca taaacaacat gggattgatg tcattgcgta tggaaattca  1574

ttacatgata ttgacagcta ttatttaatc cgtgcatttg agacagaaac caaattgcaa  1634

cagcagctcg atgctttta tgccagtgat gattggcgtg atggaccaag agaaagtatc   1694

attcgcctga ttgaaagcag tttaaaatcg gtgatcatgc tcccgacaca ggcaatccat  1754

gcactacgca accattatcc tcaataaaat caacaaccgc acccaatcag tgcggtcatt  1814

ttttcttact ttttcagtgc taagggaaaa acaacgatag tggacgttgt ttaatcaatt  1874

tccaaacaca ttgcgcgata tcacaccaac tctcaatttc tgtttctaaa gaacgcagcg  1934

caacccataa cgcgataaag aaactgacaa tcaaattcac cataccaatc aataacacga  1994

acactaaacc ttgtaagaac atctgccaag taaacgcgcc actgatcgcc atatagccca  2054

aattcgcaga agaaacgcc acatggcgaa tatctaacgg taaattaagc aaatacccga   2114

ctaaccccgt aaaccaagc aataaaccaa aacacagatt tcccataatc gaaccgtaat   2174


                                 158
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tatcatgcca gtattctgca aatttgtagc gcatattacg ggtcaacaga cggcgtaaaa 2234

tagggtgatt tcttagtcgc atttttaagt tcaaataatt actacgatta tcaaaataac 2294

cagaaataat cccagaaaag aataaccaga aacccgcaat ggcggcaaac cataaggacc 2354

ctttcatcgg atcaagggat ttttgttggt aggcaatctc cgcgtcactc aataaaggtg 2414

taccaacata atgttgatag cctagcgcaa gcaaacaagc cacagaaatc gctaaagtga 2474

cattacccaa gactgccact gtttgcgagc gaaacacatc gatcagcagt tgagctaatt 2534

gcagattaac ggatttgcct tgtccattat ccaccgtttc tgcaaaacgt gctgca     2590
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<210> 79
<211> 129
<212> PRT
<213> Pasteurella multocida

<400> 79

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Met Thr Lys Val Ile His Thr Asp Asn Ala Pro Ala Ala Ile Gly Pro
 1               5                  10                  15

Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser Gly Gln
            20                  25                  30

Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile Val Ala
        35                  40                  45

Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu Gln Ala
    50                  55                  60

Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val Lys Asp
65                  70                  75                  80

Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe Phe Lys
                85                  90                  95

Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu Val Ala
            100                 105                 110

Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Lys
        115                 120                 125

Ala
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<210> 80
<211> 6642
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (463)..(1884)

<220>
<223> yleA

<400> 80
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159

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aacccagctc agataagttt aattctggct atggaaagtg gaccaaatcc ttcgatctcc 60

caggtttcta aggcgcgata cgggcaaata cgagtatttt cgatatactg ccaagcacct 120

agttgtttta agagattaac ggaagcaaca ctgatcgcag aaatgcgaag atcgtaaggc 180

gaattaggtt gaaactgtgg gagtggggcg tgttcgataa gctggacttg atgtccttgt 240

ttacgtaagc caagcgcaca ggctgcacca accatgccac cgccaaccac gatcatgtct 300

ttttgtatga cgtccatagg attttccttt tcttttttgtt acgtattcta ccgtcaatga 360

gggaatttca aaagaaatct cttttttagc tagccagcat aggttcaaga ctgtaaaata 420

gtcagtcaca tttttatagg ttaactgaat tttttaaacg at atg acg caa aaa      474
                                              Met Thr Gln Lys
                                                1

tta cat att aaa acg tgg ggt tgt cag atg aat gaa tat gat tca tct     522
Leu His Ile Lys Thr Trp Gly Cys Gln Met Asn Glu Tyr Asp Ser Ser
  5              10                  15                  20

aaa atg gca gat ctc tta aac agt act cac ggc tta gag tta aca gaa     570
Lys Met Ala Asp Leu Leu Asn Ser Thr His Gly Leu Glu Leu Thr Glu
                  25                  30                  35

att ccg gaa gaa gcg gat gtg tta ttg tta aac act tgc tca att cgt     618
Ile Pro Glu Glu Ala Asp Val Leu Leu Leu Asn Thr Cys Ser Ile Arg
              40                  45                  50

gaa aaa gca caa gaa aaa gtt ttc cat caa tta gga cgt tgg aaa gaa     666
Glu Lys Ala Gln Glu Lys Val Phe His Gln Leu Gly Arg Trp Lys Glu
          55                  60                  65

tta aag aaa cat aag ccg gga ctc gtt atc ggt gtt ggg ggc tgt gtt     714
Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val Gly Gly Cys Val
      70                  75                  80

gcc tca caa gaa gga gaa cac att cgt act cgt gct cct tat gtc gat     762
Ala Ser Gln Glu Gly Glu His Ile Arg Thr Arg Ala Pro Tyr Val Asp
  85                  90                  95                  100

att att ttt gga cca caa acc tta cat cgt tta cct gaa atg atc aat     810
Ile Ile Phe Gly Pro Gln Thr Leu His Arg Leu Pro Glu Met Ile Asn
                  105                 110                 115

cag atc aga ggt ggt aaa agc tca gta gtc gat gtc agt ttt cca gaa     858
Gln Ile Arg Gly Gly Lys Ser Ser Val Val Asp Val Ser Phe Pro Glu
              120                 125                 130

att gaa aaa ttc gac cgt tta cca gaa ccg cgt gca gaa ggt cca act     906
Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala Glu Gly Pro Thr
              135                 140                 145

gct ttc gta tcc att atg gaa ggc tgt aat aaa tat tgc tca ttc tgt     954
Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr Cys Ser Phe Cys
          150                 155                 160

gtc gtg cct tat acg cgt ggt gaa gaa gtc agt cgt cca gtg gat gat     1002
Val Val Pro Tyr Thr Arg Gly Glu Glu Val Ser Arg Pro Val Asp Asp
165                 170                 175                 180
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160

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gta tta ttt gaa att gca cag ttg gca gag caa ggc gtg cgt gaa gtg    1050
Val Leu Phe Glu Ile Ala Gln Leu Ala Glu Gln Gly Val Arg Glu Val
                185             190             195

aat tta tta gga caa aac gtg aac gct tat cgt ggt gca act cat gat    1098
Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly Ala Thr His Asp
                200             205             210

gac ggt att tgt act ttt gcg gaa ttg tta cgt tta gta gcc gct att    1146
Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu Val Ala Ala Ile
                215             220             225

gat ggt att gac cgt tta cgt ttt acc acc agt cac cca att gag ttc    1194
Asp Gly Ile Asp Arg Leu Arg Phe Thr Thr Ser His Pro Ile Glu Phe
                230             235             240

act gat gac att att gat gtg tac cgt gat acg cca gag ttg gtg agt    1242
Thr Asp Asp Ile Ile Asp Val Tyr Arg Asp Thr Pro Glu Leu Val Ser
245             250             255             260

ttc tta cac tta cct gta caa agt ggt tct gat cgt gtg tta tct atg    1290
Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg Val Leu Ser Met
                265             270             275

atg aaa cgc aat cat acg gca tta gaa tat aaa tcg att att cgg aag    1338
Met Lys Arg Asn His Thr Ala Leu Glu Tyr Lys Ser Ile Ile Arg Lys
                280             285             290

tta aga gcg gtg cgt cca gag att caa att agc tca gat ttt att gtc    1386
Leu Arg Ala Val Arg Pro Glu Ile Gln Ile Ser Ser Asp Phe Ile Val
                295             300             305

ggt ttc ccg ggc gaa aca gca gaa gat ttc gag caa acc atg aat tta    1434
Gly Phe Pro Gly Glu Thr Ala Glu Asp Phe Glu Gln Thr Met Asn Leu
                310             315             320

att gca caa gta aat ttt gat atg agt ttc agc ttc att tat tca gca    1482
Ile Ala Gln Val Asn Phe Asp Met Ser Phe Ser Phe Ile Tyr Ser Ala
325             330             335             340

cgt cca ggc acg cca gca gca gat atg cct gat gat gtg aca gaa gaa    1530
Arg Pro Gly Thr Pro Ala Ala Asp Met Pro Asp Asp Val Thr Glu Glu
                345             350             355

gag aag aaa caa cgt tta tat gtg ttg caa caa cgc att aac aat caa    1578
Glu Lys Lys Gln Arg Leu Tyr Val Leu Gln Gln Arg Ile Asn Asn Gln
                360             365             370

gcc gcg caa ttt agt cga gca atg tta ggc aca gaa cag cgc gtg tta    1626
Ala Ala Gln Phe Ser Arg Ala Met Leu Gly Thr Glu Gln Arg Val Leu
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gtg gaa gga ccc tcg aaa aaa gat tta atg gaa ctc aca ggg cgt aca    1674
Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu Thr Gly Arg Thr
                390             395             400

gaa act aat cgt atc gtc aat ttt gtg ggc acg cct gat atg att ggg    1722
Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro Asp Met Ile Gly
405             410             415             420

aag ttt gtt gat atc aag atc acg gat gtg ttt act aac tca ctg cgt    1770
Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr Asn Ser Leu Arg
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161

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ggt gaa gtc gtt aga act gaa gaa caa atg gga ctt cgc gtt gtt caa    1818
Gly Glu Val Val Arg Thr Glu Glu Gln Met Gly Leu Arg Val Val Gln
             440                    445                    450

tcg cca caa atg gtg att aat cgt act cgt aaa gaa gat gaa ctc ggc    1866
Ser Pro Gln Met Val Ile Asn Arg Thr Arg Lys Glu Asp Glu Leu Gly
         455                    460                    465

gtg gga cgt tat cac gcg tagtcgtgct atcccttcaa atatttaacc    1914
Val Gly Arg Tyr His Ala
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162

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163

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cgcacgccta ggataagcaa ataaatgggt aatccaatca atgcggtata ttttgcttgg  5514

cagaaaagcg ataaaccaat taactcggga ataatgttta agaaataatt cgggtgacgt  5574

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Tyr Asp Ser Ser Lys Met Ala Asp Leu Leu Asn Ser Thr His Gly Leu
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Glu Leu Thr Glu Ile Pro Glu Glu Ala Asp Val Leu Leu Leu Asn Thr

164

Cys Ser Ile Arg Glu Lys Ala Gln Glu Lys Val Phe His Gln Leu Gly
        50   55   60

Arg Trp Lys Glu Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val
65   70   75   80

Gly Gly Cys Val Ala Ser Gln Glu Gly Glu His Ile Arg Thr Arg Ala
                85   90   95

Pro Tyr Val Asp Ile Ile Phe Gly Pro Gln Thr Leu His Arg Leu Pro
            100   105   110

Glu Met Ile Asn Gln Ile Arg Gly Gly Lys Ser Ser Val Val Asp Val
            115   120   125

Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala
    130   135   140

Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr
145   150   155   160

Cys Ser Phe Cys Val Val Pro Tyr Thr Arg Gly Glu Glu Val Ser Arg
            165   170   175

Pro Val Asp Asp Val Leu Phe Glu Ile Ala Gln Leu Ala Glu Gln Gly
            180   185   190

Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly
        195   200   205

Ala Thr His Asp Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu
        210   215   220

Val Ala Ala Ile Asp Gly Ile Asp Arg Leu Arg Phe Thr Thr Ser His
225   230   235   240

Pro Ile Glu Phe Thr Asp Asp Ile Ile Asp Val Tyr Arg Asp Thr Pro
            245   250   255

Glu Leu Val Ser Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg
            260   265   270

Val Leu Ser Met Met Lys Arg Asn His Thr Ala Leu Glu Tyr Lys Ser
            275   280   285

Ile Ile Arg Lys Leu Arg Ala Val Arg Pro Glu Ile Gln Ile Ser Ser
    290   295   300

Asp Phe Ile Val Gly Phe Pro Gly Glu Thr Ala Glu Asp Phe Glu Gln
305   310   315   320

Thr Met Asn Leu Ile Ala Gln Val Asn Phe Asp Met Ser Phe Ser Phe
            325   330   335

Ile Tyr Ser Ala Arg Pro Gly Thr Pro Ala Ala Asp Met Pro Asp Asp
            340   345   350

Val Thr Glu Glu Glu Lys Lys Gln Arg Leu Tyr Val Leu Gln Gln Arg
        355   360   365

165

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Ile Asn Asn Gln Ala Ala Gln Phe Ser Arg Ala Met Leu Gly Thr Glu
    370             375             380
Gln Arg Val Leu Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu
385             390             395             400
Thr Gly Arg Thr Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro
                405             410             415
Asp Met Ile Gly Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr
            420             425             430
Asn Ser Leu Arg Gly Glu Val Val Arg Thr Glu Glu Gln Met Gly Leu
        435             440             445
Arg Val Val Gln Ser Pro Gln Met Val Ile Asn Arg Thr Arg Lys Glu
    450             455             460
Asp Glu Leu Gly Val Gly Arg Tyr His Ala
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aacggacttc aaaaaatgtg cggtcaaagt ggaaaaagcg taacacgtta aatttaatga 360

ggaacgaccg cactttgctt tcagtaaagt gcggttggaa agtcga atg aaa aaa    415
                                                    Met Lys Lys
                                                     1

aca gtt gtg aat cct gaa cgt cgt cga ttt ttt aaa gag gct acg cgc    463
Thr Val Val Asn Pro Glu Arg Arg Arg Phe Phe Lys Glu Ala Thr Arg
     5                  10              15

act gca ggc ggg ttg gca ggg gtg act ttg ctc ctt ggt ttg caa caa    511
Thr Ala Gly Gly Leu Ala Gly Val Thr Leu Leu Leu Gly Leu Gln Gln
 20             25              30                      35

aag cag agt ctt gcg cgc gaa ggc gtg gcg tta cgc cca cct ttt gcc    559
Lys Gln Ser Leu Ala Arg Glu Gly Val Ala Leu Arg Pro Pro Phe Ala
             40              45                      50
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166

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ctt gag aat gag aaa gcg ttt tct gct gcg tgc att cgt tgt ggt cag    607
Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg Cys Gly Gln
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tgt gta caa gcc tgt cca cat gag atg ttg cat ctt gcc tca ctg att    655
Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala Ser Leu Ile
            70                  75                  80

tca ccg atg gaa gca ggt aca ccg tat ttc att gcg cgc gat aag ccc    703
Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg Asp Lys Pro
        85                  90                  95

tgt gaa atg tgt gtg gat att cct tgt gca aaa gcc tgc cca acc ggt    751
Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys Pro Thr Gly
100                 105                 110                 115

gca ttg gat aat caa gca aca gaa atc gat gat gcg cgt atg ggg tta    799
Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg Met Gly Leu
                120                 125                 130

gct gtc ctg cta gat cat gaa act tgt ctg aac tgg caa ggt tta cgc    847
Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln Gly Leu Arg
            135                 140                 145

tgt gat gtg tgt tat cgc gtc tgt ccg ctg att aat aaa gcg att acg    895
Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys Ala Ile Thr
            150                 155                 160

tta gtg atg cat cgt aat gag cgt acg ggt aag cac gcc gtc ttt atc    943
Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala Val Phe Ile
        165                 170                 175

cca aca gtg cat tcc gaa gcc tgt aca gga tgt ggc aaa tgt gaa gaa    991
Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys Cys Glu Glu
180                 185                 190                 195

gct tgc gtt cta gaa gaa gcg gca atc aaa gtg tta ccg atg gca tta   1039
Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro Met Ala Leu
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gcg aaa ggc atg tta ggt aaa cat tac cgt tta ggt tgg gaa gag aaa   1087
Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp Glu Glu Lys
            215                 220                 225

gaa aaa gcc ggg cat tcc ctt gcg cca gaa ggc att att tct ctc ccg   1135
Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile Ser Leu Pro
            230                 235                 240

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Thr Arg Leu Pro Glu Ser Leu
245                 250

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167

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168

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gcctttcaac agataggctg gacggcacag cagattcagc gttggtttac gcctgagaac 3406

cgttatattg atcccgcgtt agcctgggta aacgaacaac aacatattgt ggattggttt 3466

gatcctcatt atcctccctt gttaaagcaa acagaagagg caccacttgt cttgtttgtg 3526

aaaggggaag tggctacgct atctgcacag caagtggcga tcgtgggcag tcgtcattgt 3586

tcacgttatg gggaatactg ggcaaattat ttcgccactc aactggctta tgccgatatt 3646

gtggtgacca gtggtttagc gttaggtatt gatggtttct cacatcaagc ggtagtggat 3706

atccacggga agacgattgc agtattaggc agtggtttag aggtcattta tccgaaaaaa 3766

caccgaggtt tagccgaaaa aattattgaa catcaaggtg cgttagtgtc tgaattttta 3826

cctttccaac cccctgtggc agaaaatttt ccacgtcgta atcgcattat tagtggttta 3886

tctttgggga cattagtcat tgaagcctca gaaaacagtg gttctttaat tactgcccgc 3946

tatgctttag agcaaaatcg agatgttttt gcgttaccgg ggcagattca gcatggattt 4006

agccaaggtt gtcataaact gattaaacag ggggcaatat tagtcgaaag tattcaggat 4066

attttagaac atctctcgcc ttattcgcat tgtgccatgc cagcgttgcc tcgtacggag 4126

aacgcctttt ctcaacaagt aacagacaca tcaaccatca atactgcgcg gataacgcca 4186

gaacatccgg aattatatgc caaaattggc tatatgcccg tcagtattga tgtattagcc 4246

caacaagtca atctacctat tgatacctta ttagtacagc ttttaacctt ggaattgcaa 4306

gacttgattg ttgctgaaaa tggattatat cagcgcaaat aacggaaaga gtaaccacaa 4366

atgagaaagg actgtgttga aacggctatc aacatcagtc cttgcagtat attatctcat 4426

atgacacgag acggcagttt catgagatta atagagacta aacgcttgta aatacggtag 4486

tttgcctcgt tgtagcattt tctcaatatt gcctttgtga tcatcacgac ctaagcctcg 4546

tagctcaata ttgataccaa tacttttgtc ataaaaaatt tgattcgccg tttggttttc 4606

tttgctggtc acactacgtc gggcaccaac attaatcgcc aacagcaag tgctgtattc 4666

tagtcccaaa tattgctcaa caggctttct caacgcaaga tcttgataat gacgtgctac 4726

caccgcccat tgatccgtga gtgcccatgc cacagttaga ccaagctgtt ttatgtcttg 4786

tccgtagcgg ttcgccgctg aggtgaggtt ttggtcaata tattgttga           4835
```

<210> 83
<211> 250
<212> PRT
<213> Pasteurella multocida

<400> 83

```
Met Lys Lys Thr Val Val Asn Pro Glu Arg Arg Arg Phe Phe Lys Glu
 1               5                  10                  15

Ala Thr Arg Thr Ala Gly Gly Leu Ala Gly Val Thr Leu Leu Leu Gly
            20                  25                  30
```

```
Leu Gln Gln Lys Gln Ser Leu Ala Arg Glu Gly Val Ala Leu Arg Pro
        35                  40                  45

Pro Phe Ala Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg
        50                  55                  60

Cys Gly Gln Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala
65                  70                  75                  80

Ser Leu Ile Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg
                85                  90                  95

Asp Lys Pro Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys
            100                 105                 110

Pro Thr Gly Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg
            115                 120                 125

Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln
    130                 135                 140

Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys
145                 150                 155                 160

Ala Ile Thr Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala
                165                 170                 175

Val Phe Ile Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys
            180                 185                 190

Cys Glu Glu Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
        195                 200                 205

Met Ala Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp
    210                 215                 220

Glu Glu Lys Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile
225                 230                 235                 240

Ser Leu Pro Thr Arg Leu Pro Glu Ser Leu
                245                 250


<210> 84
<211> 3494
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (2411)..(2719)

<220>
<223> yyaM

<400> 84
gtcaacgatc cgaatacgac ggaagaaaac tatatgcaag tcatttatgg caagactgcg  60

cgtctattcg aagctgcgac gcattgcgcc gcgatacttg ctcatgcgac ggaagcccaa 120

gaaaatgctt tacgcgaata tggttgttat ctaggcacag cttttcaatt agtcgatgat 180
```

170

```
attttagatt atagtgcaga tgcaaaagca ctcggcaaaa atattggtga tgatttagcg 240

gaaggtaaac caacattacc gttattacac gccatgcatc acggcaatcc agcacaagca 300

aaattgattc gcgaagcgat tgagcaaggg ggtaagcgtg atattttaga ggatgtactg 360

acaattatga cagaacataa atccctcgac tatgcgatga tgcgcgctaa acaagaagca 420

caaaaagccg ttgatgcgat tgcattattg cctgaaaatg aatataaaca agcgttaatt 480

tcattagctt acttatccgt cgatcgcgct tattaaccac ttaataaggc gagacatgtt 540

agcgtaacga ccgcctaaag tgcggtcatt tatttagtaa ttttaaacac gacaatgaca 600

gaacaaaaca tccctacgaa aaaaacacgc aaaggcaaag atcctcacgc gccttttgta 660

cgcgaaaaat tatccctacc aaatgggcat aacaaattgt tattgcattc ttgttgtgcg 720

ccttgctcgg gagaagtaat ggaggcaatt catgcttcag gtattgaatt tactatttac 780

ttctacaacc caaacattca cccattaaaa gaatatctca ttcgtaaaga agaaaatatt 840

cgttttgcgg aaaaatgggg cattccgttt attgatgccg attatgatcg tcaagaatgg 900

tttgaccgtg ccaaaggcat ggaagatgag ccagagcgtg gtattcgttg cactatgtgc 960

tttgatatgc gttttgaaaa agccgcagaa tatgcacaca caatggttt ccccgtattt 1020

actagctgct taggtatttc acgttggaaa gacatgaacc aaatcaacgg ttgtggacac 1080

cgtgccgccg aaaaatatga tgatgtagtg tattgggatt ataactggcg taaaggtggt 1140

ggctcacaac gtatgattga aatcagtaag cgtgaacgtt tttaccagca agaatattgc 1200

ggttgtgtgt attctttgcg tgacacgaat aaatggcgtg aagcaaacgg acgccaaaaa 1260

attgaaattg gcaaattgta ttattccgcc gattaaaaca accaagtaaa ccatcgtgcc 1320

gtcatataac atggcggcac ttttttaggc tttatatatg caacgttttc gccaatcttt 1380

cgaaacctaa tgctaacgcc tcttcactaa tatttaatgc tggggcaaaa cgcaatacat 1440

taggacccgc cactaaaatc attaagccat tatctgctgc ttttttgaca aattcgctcg 1500

ctcttccgtg atattgctcg ataagttctg caccaattaa caaaccttcg ccacggattt 1560

ctttaaataa gccacattgc tgattaattt cttgcagctt ttgcataaat ttttcagaag 1620

tgcgctgaat tttttgcaag aatggtggtg ctgaaatgat atcaatcact ttttctgcca 1680

cggcacaagc gagaggattg ccaccaaagg tggtgccatg cacgccaggt gcaaaacttt 1740

tggcgatctc atgcgttgtc aacgaatgag aaaattgtga cagattgggc tccaacggga 1800

cgtgcggatg agattgggga tacgcaagta cgttatgaaa ttgagcaggt gagttctagc 1860

aattatagtg cactgtttgt ctccatttta cagatgaaac gtaatgaggt ggtatttagt 1920

ccacatttag cggataaaca acgttatagt tctgatcgct tgaaccaact tgttggtgaa 1980

ttagatgcgt cttatcgtaa acaagtccgt gatttgaata acagcggatt gatgccaatt 2040
```

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cagtctgtat tcggtacgga cagtaatggg cgtactgctc tcgtgttagg cgcacccttt 2100

aatcatgcgt ggacaaaact aggacaagtt ttaccgcagc ttgaatttga tattaaagat 2160

gaaattattg gtcgtggggt aagggagtta aaataccgtc cagctggagc aaaaagttgg 2220

tggtggccat ttggtcgtgc tgaaggcagt agcggactga aaacaggtac ctattttatg 2280

cagttaagcg ccttagggaa gcaaagtgcg gtggtgatga ccgatgatga tggcaatgcg 2340

ttatctgggg agcaagctca ggcgctttat caagcattac aaaatctctt agcgaaataa 2400

tacagtcaag atg act aaa ctc agt atc cag cga gat aac ttg att tgt   2449
          Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys
            1   5   10

ttg agt tat gtc gca tta atg gga ttc ggc ttt ccc att atg cgt tat   2497
Leu Ser Tyr Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr
    15   20   25

atg agt att cat ttt gat aca tta aat aat aac gct gtt cgc ttt ctc   2545
Met Ser Ile His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu
 30   35   40   45

tca ggg ggc agc gtt ttt att tta gcc tgt ttt ttt tat tat cgc gct   2593
Ser Gly Gly Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala
                50   55   60

gag tta aca tct tcg ggg gct ggc gtc cag tcc gtt gcg atg ttg ccg   2641
Glu Leu Thr Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro
            65   70   75

agt tca agt tta ggt ttc tta ata ttg aaa act gta cca tct ttt tca   2689
Ser Ser Ser Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser
        80   85   90

tac gtt aca atc tca aca ctt aat cgc gtt tgaccttccg atttttgata   2739
Tyr Val Thr Ile Ser Thr Leu Asn Arg Val
    95   100

gtcaaagact actgagtaac gcttgtagtc gcgtgaatcg actgttacat aagccgatat 2799

gtcagaataa gtactgccgg tatatcgtct taatctaaga ttaagcttgc cacttttgtt 2859

cgataaagcg tcaaacgaaa gcacgacttt accgtccttg acttccacct gatcttcaat 2919

gagcacttga cttagtgcga ccaatcgacc gttggcagtc agtgtcgcaa tgccgtgatc 2979

cgtatcaagc gttacaccgc tattttttcc ccagttttta ttgagctttt cactatgttt 3039

cagtaagttt ctgccaccaa tctgcaactg attaaactta gcttcaagcg tttcactctt 3099

gactgcaagc gacttgtttt cattgctaac cgtctgctca agtgctgtga ttttggatgt 3159

taaatctaac ttagttgcat tgacttcatc agtccattct gactttaact cttttctcgc 3219

aagtgacgcc acttcatctt tgctagcttt cgtttctttt aagtcagaaa tgccactagt 3279

attttgcgcc actttagaat cgagcgtttc tagttttgta gagaaagatt tgtctttttc 3339

gctagccgtt ttttgaatta gctgtatttc actttcgctc aatccaactc tagcagttag 3399

172

actgtctagc ttgtcagcag tagatttatt cacagtcgct tgtgattgct tgtgttgaat 3459

aatatccgcg cttacttccg agatagccac gtcga   3494

<210> 85
<211> 103
<212> PRT
<213> Pasteurella multocida

<400> 85
Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys Leu Ser Tyr
 1   5   10   15

Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr Met Ser Ile
            20   25   30

His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu Ser Gly Gly
        35   40   45

Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala Glu Leu Thr
     50   55   60

Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro Ser Ser Ser
 65   70   75   80

Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser Tyr Val Thr
                85   90   95

Ile Ser Thr Leu Asn Arg Val
            100

<210> 86
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 86
aggccggtac cggccgcct   19

<210> 87
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 87
cggccggtac cggcctagg   19

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

```
<220>
<223> Description of Artificial Sequence: primer

<400> 88
catggtaccc attctaac                                              18


<210> 89
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 89
ctaggtacct acaacctc                                              18


<210> 90
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: transposon
      insert

<400> 90
ctaggtacct acaacctcaa gcttnknknk nknknknknk nknknknknk nknknknknk 60

nknknknknk nknknknknk nknknknknk nknkaagctt ggttagaatg ggtaccatg  119


<210> 91
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 91
tacctacaac ctcaagct                                              18


<210> 92
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 92
tacccattct aaccaagc                                              18


<210> 93
<211> 19
<212> DNA
<213> Artificial Sequence
```

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<220>
<223> Description of Artificial Sequence: primer

<400> 93
tacctacaac ctcaagctt   19

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 94
tacccattct aaccaagctt   20

<210> 95
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 95
ggcagagcat tacgctgac   19

<210> 96
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 96
gtaccggcca ggcggccacg cgtattc   27

<210> 97
<211> 531
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> atpG

<400> 97
tgttgagctt ggtttagtag ggtcgaaagg cgtaagcttt taccaaaatc taggcttaaa 60

cgtgagatct caagtaacgg gattaggcga taatccggaa atggaacgta tcgtgggcgc 120

agttaatgaa atgattaatg cgttccgaaa cggagaagtg gatgcggttt acgtcgctta 180

caaccgtttt gaaaatacga tgtcacaaaa acctgttatc gcacagttac ttccgttacc 240

taaactagat gacgatgaat tagatacgaa aggttcatgg gattatattt atgaaccgaa 300

175

```
tccacaagtt ttattggata gtttacttgt tcgttattta gaaactcagg tataccaagc 360

agttgtagat aacctagctt ctgaacaagc cgctcgaatg gtagcgatga aagccgcaac 420

agataatgcg ggtacattaa tcgatgaatt acaattagtg tataacaaag ctcgccaagc 480

aagcattaca aatgaattaa acgaaattgt tgcgggtgcc gcagcaattt a        531
```

<210> 98
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 98
```
tctccattcc cttgctgcgg caccc                                        25
```

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 99
```
ggattacagc cggatccggg                                              20
```

<210> 100
<211> 1034
<212> DNA
<213> Pasteurella multocida

<220>
<223> cap5E

<220>
<221> CDS
<222> (1)..(1032)

<400> 100
```
atg ttt aaa aat aaa aca ctt tta att aca ggt gga acg ggt tct ttt   48
Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe
 1               5                  10                  15

ggt aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att   96
Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile
            20                  25                  30

cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cgg aaa aaa   144
Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys
        35                  40                  45

tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac   192
Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr
    50                  55                  60
```

```
gat agt att tta aat gcc tcg cga ggt gtt gac tat att tat cat gct    240
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala
 65                      70                  75                  80

gcc gca tta aag caa gtg cct tca tgc gag ttt tat ccg tta gag gca    288
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala
                    85                  90                  95

gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc    336
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile
                   100                 105                 110

caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg    384
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val
                   115                 120                 125

tac cca att aat gcg atg ggc att tct aaa gca atg atg gaa aaa gtc    432
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val
               130                 135                 140

atc atc gca aaa tcg cgt aac cta gaa ggc aca cca acg aca atc tgt    480
Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys
145                 150                 155                 160

tgt act cgc tat ggc aat gtc atg gca tcg cgt ggt tcg gtt atc cca    528
Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro
                   165                 170                 175

tta ttt gtc gat caa ata cgt caa ggc aag cct ttt act att act gat    576
Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp
               180                 185                 190

cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta    624
Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu
               195                 200                 205

gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa    672
Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln
               210                 215                 220

aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa    720
Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu
225                 230                 235                 240

tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat    768
Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His
               245                 250                 255

gga gag aaa gca ttc gaa gct tta tta agc cgt gaa gaa atg gtt cat    816
Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His
               260                 265                 270

gca att aat gaa ggt aat tat tat cgc atc cca gcc gat caa cgc agt    864
Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser
               275                 280                 285

tta aat tac agt aaa tat gtc gaa aaa ggg gaa cca aaa att acc gaa    912
Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu
               290                 295                 300

gtc acc gac tac aac tca cat aat act gag cgt ttg act gtc aag gaa    960
Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu
```

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```
atg aag cag tta ctg ctt aaa ctt gaa ttc ata cag aaa atg att gag    1008
Met Lys Gln Leu Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu
                325                 330             335
```

```
ggt gaa tac atc tca ccg gag gta ta                                 1034
Gly Glu Tyr Ile Ser Pro Glu Val
            340
```

<210> 101
<211> 344
<212> PRT
<213> Pasteurella multocida

<400> 101

```
Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe
1               5               10              15

Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile
            20              25              30

Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys
        35              40              45

Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr
    50              55              60

Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala
65              70              75              80

Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala
                85              90              95

Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile
            100             105             110

Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val
        115             120             125

Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val
    130             135             140

Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys
145             150             155             160

Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro
            165             170             175

Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp
            180             185             190

Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu
            195             200             205

Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln
    210             215             220

Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu
225             230             235             240
```

```
Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His
            245             250             255

Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His
            260             265             270

Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser
            275             280             285

Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu
            290             295             300

Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu
305             310             315             320

Met Lys Gln Leu Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu
            325             330             335

Gly Glu Tyr Ile Ser Pro Glu Val
            340
```

<210> 102
<211> 4931
<212> DNA
<213> Pasteurella multocida

<220>
<223> fhaB2

<220>
<221> CDS
<222> (1)..(4929)

<400> 102
```
atg aac aaa aat cgt tac aaa ctc att ttt agt caa gtc aaa ggt tgt    48
Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys
 1               5                  10                  15

ctc gtt cct gtg gca gaa tgt att aac tca gct att agc aat ggt tca    96
Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser
                20                  25                  30

tct gat tca aca tcc aca tca gaa caa gtt gaa gag gaa cct ttc ctt   144
Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
            35                  40                  45

cta gaa caa tat tca ctt tcc tcc gtg tct tta tta gta aaa agc acg   192
Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
    50                  55                  60

ttc aat cct gtt tcg tat gca atg caa ttg act tgg aaa cag ctt tct   240
Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
65                  70                  75                  80

att tta ttt tta act gtg att tct gtt cct gtt ttg gct gag gga aaa   288
Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
                85                  90                  95

ggg gat gaa aga aat caa tta aca gtg att gat aat agc gat cat att   336
Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
            100                 105                 110
```

179

aaa tta gat gca tct aat ctt gct ggt aat gat aaa aca aaa atc tat   384
Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
            115   120   125

caa gca gaa aat aaa gtt ctg gtt att gat att gct aaa cca aat ggg   432
Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
       130   135   140

aaa ggg att tca gat aac cgt ttt gaa aaa ttt aat att cca aat agc   480
Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
145   150   155   160

gcg gtg ttt aat aat aat ggg act gaa gcg cag gca aga tca aca tta   528
Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
            165   170   175

att ggt tac att ccg caa aat caa aat tta agg gga ggg aaa gaa gct   576
Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
            180   185   190

gat gtt ata tta aat caa gtg aca ggt cct caa gaa agt aaa att gtt   624
Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
            195   200   205

ggc gcg ctt gaa gta tta ggt aaa aaa gct gat atc gtc att gca aac   672
Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
            210   215   220

caa aat ggt att acc tta aat ggt gta aga aca ata aat tca gat cgt   720
Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
225   230   235   240

ttt gtt gcc act acg agt gag ctt ata gat ccg aat cag atg atg tta   768
Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
            245   250   255

aag gtt aca aaa gga aat gtg atc att gat att gat ggt ttt tcg aca   816
Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
            260   265   270

gat gga tta aag tat tta gat att att gct aaa aaa att gaa caa aag   864
Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
            275   280   285

caa tca att aca tca ggg gat aat tca gaa gca aaa aca gat gtc act   912
Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
            290   295   300

ctt att gcg ggt tcc agt gaa tat gat tta agc aaa cat gag ctg aaa   960
Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
305   310   315   320

aaa acg agc ggt gaa aat gta tct aat gat gtt att gct atc acg gga 1008
Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
            325   330   335

tct agt aca ggc gca atg cat ggt aaa aat att aag ttg att gtg aca 1056
Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
            340   345   350

gat aaa ggt gca ggc gta aaa cat gat gga att att ttg tct gaa aat 1104
Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn

180

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gat att cag att gaa atg aat gaa ggt gac tta gaa ctt ggc aat acg    1152
Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
    370             375             380

att cag caa aca gtg gta aaa aaa gac cga aat att cga gcc aag aaa    1200
Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
385             390             395             400

aaa att gaa gtg aaa aac gct aat cgt gtt ttt gtt ggt agt caa acg    1248
Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
            405             410             415

aaa tca gat gaa att tcg tta gag gcg aaa caa gtt aaa atc aga aaa    1296
Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
        420             425             430

aac gca gag att agg agt acg aca caa gcc aaa atc gta gca aag ggt    1344
Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
        435             440             445

gcc ctg tct att gag caa aat gcg aag ctc gtc gct aaa aag ata gat    1392
Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
    450             455             460

gtg gca aca gaa act cta act aat gct ggg cgt att tat ggt cga gag    1440
Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
465             470             475             480

gtt aag ctt gac act aat aat ttg att aat gat aaa gaa att tat gct    1488
Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
            485             490             495

gaa cgg aaa ttg agt att ttg acg aaa gga aaa gat ctt gaa att att    1536
Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
        500             505             510

caa gat aga tat ttg tct cca ctg atg cgc gta aaa agt agt gtc cgc    1584
Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
        515             520             525

ttt tta ggc tct ccg ttt ttc tca ata tct ccg tcg atg ctc gca agc    1632
Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
    530             535             540

ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa    1680
Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
545             550             555             560

agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta    1728
Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
            565             570             575

aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac    1776
Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn
            580             585             590

gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct    1824
Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala
        595             600             605
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181

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aat ata acg ttg aat gtg gaa gaa aac ttt gtt aat cgt gca gga aca       1872
Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr
    610             615             620

ctg gca act ggt aaa aca ctg aca att aat acc gaa agt ggc agt att       1920
Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
625             630             635             640

tac aat ctt ggt ggg aca tta ggt gct gga aaa tca tta aaa ctg act       1968
Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
            645             650             655

gct aaa tca acg gaa gaa ggt atg gga aat att gtt aac caa gaa aac       2016
Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
            660             665             670

ggt tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag cgt tct       2064
Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
            675             680             685

gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca gtt cat       2112
Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His
    690             695             700

act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg agt tat       2160
Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
705             710             715             720

aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt gcg gta       2208
Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
            725             730             735

cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg caa gaa       2256
His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
            740             745             750

caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc cgt tct       2304
Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
            755             760             765

gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca gaa tca       2352
Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
    770             775             780

aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga aca ttt       2400
Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
785             790             795             800

aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt aac caa       2448
Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln
            805             810             815

aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg atg tac       2496
Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr
            820             825             830

tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt aat gca       2544
Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala
            835             840             845

tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg ttt ggc       2592
Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly
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182

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tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat ttt agt    2640
Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser
865              870              875              880

gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa    2688
Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys
                885              890              895

gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc tat gat    2736
Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp
                900              905              910

gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca gat ttc    2784
Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe
            915              920              925

att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa cta gaa    2832
Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu
        930              935              940

ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt ggt aag    2880
Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
945              950              955              960

ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta cca tca    2928
Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser
                965              970              975

gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa gag gac    2976
Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp
            980              985              990

ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca aac tta    3024
Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu
            995              1000             1005

ttt att gat aat agt atc caa tta gaa aag aaa aag ttg tct cct att    3072
Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile
    1010             1015             1020

gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa gaa agc    3120
Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser
1025             1030             1035             1040

cat tct aat tca tcg gat gac gtg ctt agc atg aat gat gat gag tct    3168
His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser
            1045             1050             1055

gat aca gac gat agc aag tgg agt atg ggc aat gat gag aaa gag atg    3216
Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met
            1060             1065             1070

ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca    3264
Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro
        1075             1080             1085

cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt    3312
Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe
    1090             1095             1100
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183

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gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga gaa gag      3360
Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu
1105                1110                1115                1120

ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc aat cta      3408
Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu
            1125                1130                1135

gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa      3456
Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys
        1140                1145                1150

gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag      3504
Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
        1155                1160                1165

tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa gca aga      3552
Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
    1170                1175                1180

ata gaa aaa gca ctt cta caa aaa tca gaa caa caa gaa aaa cgt gtt      3600
Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val
1185                1190                1195                1200

gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa att gct      3648
Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala
            1205                1210                1215

aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa att cgc      3696
Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg
            1220                1225                1230

cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag aag aaa      3744
Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys
        1235                1240                1245

caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct gaa cag      3792
Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln
    1250                1255                1260

aaa caa aaa gct gag gag aaa gtt gca caa gaa aga tta gac att gaa      3840
Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu
1265                1270                1275                1280

caa cag aaa gcg tat gaa gaa atg gcg aag cga gag gca gag gca tca      3888
Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser
            1285                1290                1295

aaa aat gtt tta ttg aaa gcg att gat gaa gaa cgt cca aaa gtg gaa      3936
Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu
            1300                1305                1310

act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa gat gac      3984
Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp
        1315                1320                1325

tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat aca aaa      4032
Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys
    1330                1335                1340

ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa      4080
Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln
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184

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gtg att act cgc tcg att gag aaa aaa gta gat aac cac ctt aac caa    4128
Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln
            1365                1370                1375

aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg gac aat    4176
Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn
            1380                1385                1390

tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg gca tta    4224
Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu
            1395                1400                1405

act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg tat gtc    4272
Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val
            1410                1415                1420

aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt tat ttc    4320
Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe
1425                1430                1435                1440

gct tct gaa acg ctc gta gaa gcc caa aaa tta caa ggt tta ggc act    4368
Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr
                1445                1450                1455

ggg act atc aga gtt ggt gaa gct aag att aaa gcc aaa gat gtg gtg    4416
Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val
            1460                1465                1470

aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg agt aat    4464
Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn
            1475                1480                1485

aaa atc aaa aat caa ggg agt atc tta agt act caa gaa aca cgt tta    4512
Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu
        1490                1495                1500

gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca aat gat    4560
Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp
1505                1510                1515                1520

gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa ggt cat    4608
Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His
            1525                1530                1535

tta cat ctt gaa aca gat aag gat tca act att gat gta caa gca tcg    4656
Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser
            1540                1545                1550

gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg aat ctc    4704
Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
        1555                1560                1565

aaa aat aca tac aat act aaa cat gcc tac cgt gag aaa ttc tcg ccg    4752
Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
        1570                1575                1580

agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa gtc cca    4800
Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
1585                1590                1595                1600
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ctt tta ggc gtg tcc gtc tcc atc cag ttt att cag agc ata cta gtg       4848
Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
            1605                    1610                1615

agg caa ctt caa gag gga tca atc ttc gaa gta ggg cac tta cat ntt       4896
Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
            1620                    1625                1630

gcg gta gac aga aga tgt gaa cca agc ggg gag ta                        4931
Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu
            1635                    1640


<210> 103
<211> 1643
<212> PRT
<213> Pasteurella multocida

<400> 103
Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys
 1               5                  10                  15

Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser
            20                  25                  30

Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
            35                  40                  45

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
    50                  55                  60

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
 65                  70                  75                  80

Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
                85                  90                  95

Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
            100                 105                 110

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
            115                 120                 125

Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
    130                 135                 140

Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
145                 150                 155                 160

Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
                165                 170                 175

Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
            180                 185                 190

Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
            195                 200                 205

Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
    210                 215                 220

Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
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186

Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
                    245   250   255

Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
                260   265   270

Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
            275   280   285

Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
    290   295   300

Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
305   310   315   320

Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
                325   330   335

Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
                340   345   350

Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
        355   360   365

Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
    370   375   380

Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
385   390   395   400

Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
                405   410   415

Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
        420   425   430

Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
        435   440   445

Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
    450   455   460

Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
465   470   475   480

Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
                485   490   495

Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
            500   505   510

Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
        515   520   525

Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
    530   535   540

Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
545   550   555   560

Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
            565   570   575

Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn
            580   585   590

Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala
            595   600   605

Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr
    610   615   620

Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
625   630   635   640

Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
            645   650   655

Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
            660   665   670

Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
            675   680   685

Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His
            690   695   700

Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
705   710   715   720

Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
            725   730   735

His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
            740   745   750

Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
            755   760   765

Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
            770   775   780

Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
785   790   795   800

Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln
            805   810   815

Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr
            820   825   830

Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala
            835   840   845

Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly
    850   855   860

Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser
865   870   875   880

Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys
            885   890   895

188

```
Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp
            900                     905                 910

Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe
            915                 920                 925

Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu
        930                 935                 940

Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
945                 950                 955                 960

Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser
                965                 970                 975

Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp
            980                 985                 990

Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu
            995                 1000                1005

Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile
    1010                1015                1020

Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser
1025                1030                1035                1040

His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser
                1045                1050                1055

Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met
            1060                1065                1070

Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro
            1075                1080                1085

Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe
    1090                1095                1100

Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu
1105                1110                1115                1120

Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu
            1125                1130                1135

Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys
            1140                1145                1150

Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
            1155                1160                1165

Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
    1170                1175                1180

Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val
1185                1190                1195                1200

Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala
            1205                1210                1215

Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg
            1220                1225                1230
```

189

```
Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys
         1235              1240              1245

Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln
         1250              1255              1260

Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu
1265              1270              1275              1280

Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser
         1285              1290              1295

Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu
         1300              1305              1310

Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp
         1315              1320              1325

Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys
    1330              1335              1340

Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln
1345              1350              1355              1360

Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln
         1365              1370              1375

Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn
         1380              1385              1390

Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu
         1395              1400              1405

Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val
    1410              1415              1420

Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe
1425              1430              1435              1440

Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr
         1445              1450              1455

Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val
         1460              1465              1470

Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn
         1475              1480              1485

Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu
         1490              1495              1500

Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp
1505              1510              1515              1520

Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His
         1525              1530              1535

Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser
         1540              1545              1550

Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
    1555              1560              1565
```

190

```
Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
   1570                1575                1580

Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
1585                1590                1595                1600

Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
                1605                1610                1615

Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
                1620                1625                1630

Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu
           1635                1640


<210> 104
<211> 2009
<212> DNA
<213> Pasteurella multocida

<220>
<223> hmbR

<220>
<221> CDS
<222> (1)..(2007)

<400> 104
atc cgt ggc gtt gat aaa gat cgt gtc gct gtt att gtt gat gga ata      48
Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
  1               5                  10                  15

ccg cag gct gaa tcg act ata tct act tcc gca cgt tat tcg act gaa      96
Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
               20                  25                  30

cgt cat aat ggt aat att aat aat att gaa tac gaa aat gtt agt tcg     144
Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
           35                  40                  45

ttg aaa gtt caa aaa ggg gca gct tct gta atg tat ggt agc ggt gcg     192
Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
       50                  55                  60

tta ggt gga acc gtg gag ttt acc aca aaa gat att gag gac ttt gtc     240
Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
 65                  70                  75                  80

gaa cct ggt cgc cat ttg ggc ttt ttg tct aaa acc ggc tat act tca     288
Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
               85                  90                  95

aaa aac aga gaa tat cgt caa gtc atc gga gtt gga ggg aaa ggg gaa     336
Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
               100                 105                 110

cac ttt ttt ggt ttt gta caa tta acc aaa cgt tgg ggg cat gaa aca     384
His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
           115                 120                 125

atc aac aac ggc aaa ggt aca gac att ctc ggc gaa cat cga ggt aaa     432
```

191

```
Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
    130             135             140

ccc aat ccg ctc aac tac tat act aca tca tgg tta acg aaa gtc ggt   480
Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly
145             150             155             160

tac gat att aat aac act cat cgt ttt aca ctg ttt tta gaa gat cgc   528
Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
                165             170             175

cgt gaa aag aag ctt acc gaa gaa aaa aca tta ggg ctt agt gat gca   576
Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
            180             185             190

gtg cgt ttt gct aat gat caa acc cct tat ctc cgt tat ggt att gaa   624
Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu
            195             200             205

tat cga tat aac ggc ttg tct tgg ttg gaa acg gta aag ctt ttt ttg   672
Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu
    210             215             220

gca aag cag aaa atc gaa caa cgt tct gct ctc caa gag ttt gat att   720
Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile
225             230             235             240

aat aat agg aat aaa ttg gat tcg act atg tcg ttt gta tat tta caa   768
Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln
                245             250             255

aga cag aat ata gct cgg gga gaa ttt tca acg agt cct tta tat tgg   816
Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp
            260             265             270

ggg ccg agt cgc cat cgt tta tct gcg aaa ttc gaa ttt cgt gat aag   864
Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys
            275             280             285

ttt tta gaa aat atg aat aag cat ttt acg ttt cgg ccg tgg caa atc   912
Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile
    290             295             300

aat aga ttc aga caa caa ggt cga aat aac tat aca gaa gtg ttt ccc   960
Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro
305             310             315             320

gtt aaa tcc cga gag ttt tct ttt tct ctt atg gac gac att aag att  1008
Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile
            325             330             335

ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg tgg gat cac tat aac  1056
Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn
            340             345             350

tat aag cca tta tta aat tct cag cat aat atc aac agg aca cag aga  1104
Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg
            355             360             365

tta cct tat cca aaa aca tca tcc aaa ttt tcg tat caa ttg agt tta  1152
Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu
            370             375             380
```

192

```
gag tat caa tta cat cca tca cat caa att gca tac cgt tta agt acc    1200
Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr
385             390             395                 400

ggt ttt agg gtt ccc cgt gtt gaa gat ctt tat ttt gaa gac cga gga    1248
Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly
                405             410                 415

aaa agt tct tca caa ttt ctt cct aac ccc gat cta caa ccg gaa act    1296
Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr
            420             425                 430

gca ctg aat cat gaa ata agt tac cgt ttc caa aat caa tat gcc cat    1344
Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His
            435             440                 445

ttc agc gtc ggg ctt ttc cgt aca cgt tat cat aac ttt att caa gaa    1392
Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu
    450             455                 460

cgt gag atg acc tgt gat aaa att cca tat gag tat aat agg act tat    1440
Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr
465             470             475                 480

gga tat tgc acg cat aat act tat gta atg ttt gtt aat gaa cct gaa    1488
Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu
                485             490                 495

gcc gtg att aaa ggg gtt gaa gta agc ggt gct tta aat ggg tcg gca    1536
Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala
                500             505                 510

ttc gga ctt tcc gac ggt tta act ttc cgt ctc aaa ggg agc tac agc    1584
Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser
            515             520                 525

aaa ggt caa aat cat gac ggc gat ccg tta aaa tct att caa cca tgg    1632
Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp
            530             535                 540

aca gtg gta acc ggt att gat tac gaa act gaa ggg tgg agc gtg agt    1680
Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser
545             550             555                 560

ttg agc ggg cgt tat agt gcg gct aaa aaa gcc aaa gat gcg ata gaa    1728
Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu
                565             570                 575

acg gaa tac aca cat gat aaa aag gtt gtc aaa caa tgg ccg cat tta    1776
Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
                580             585                 590

agt cca tcc tac ttt gtt gtt gat ttt acg ggg caa gtt aac ctc agt    1824
Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
                595             600                 605

aaa aat gtc att ttg aat atg ggg gta ttt aac ttg ttc aat cgt gat    1872
Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
    610             615                 620

tat atg acg tgg gac agt gca tat aac ttg ttt act agg ggg tat act    1920
Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
```

193

tcc cgt tct gtc cgt gct aac agc cca ggc att aat cgg ttt acc gca   1968
Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
            645   650   655

cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta   2009
Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
            660   665

<210> 105
<211> 669
<212> PRT
<213> Pasteurella multocida

<400> 105
Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
  1   5   10   15

Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
            20   25   30

Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
            35   40   45

Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
        50   55   60

Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
65   70   75   80

Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
                85   90   95

Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
            100   105   110

His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
            115   120   125

Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
            130   135   140

Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly
145   150   155   160

Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
                165   170   175

Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
            180   185   190

Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu
            195   200   205

Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu
        210   215   220

Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile
225   230   235   240

194

```
Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln
            245             250             255

Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp
            260             265             270

Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys
            275             280             285

Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile
            290             295             300

Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro
305             310             315             320

Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile
            325             330             335

Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn
            340             345             350

Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg
            355             360             365

Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu
            370             375             380

Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr
385             390             395             400

Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly
            405             410             415

Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr
            420             425             430

Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His
            435             440             445

Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu
            450             455             460

Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr
465             470             475             480

Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu
            485             490             495

Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala
            500             505             510

Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser
            515             520             525

Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp
            530             535             540

Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser
545             550             555             560

Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu
            565             570             575
```

195

```
Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
            580             585             590

Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
        595             600             605

Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
    610             615             620

Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
625             630             635             640

Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
                645             650             655

Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
                660             665
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<210> 106
<211> 908
<212> DNA
<213> Pasteurella multocida

<220>
<223> lgtC

<220>
<221> CDS
<222> (1)..(906)

<400> 106

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atg aat att tta ttt gtt tct gat gat gtt tat gct aaa cat ctg gtg   48
Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
  1               5              10                  15

gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt   96
Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
             20              25                  30

tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat  144
Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
         35              40                  45

gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat  192
Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
     50                  55                  60

gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta  240
Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65                  70                  75                  80

gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta  288
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
                 85                  90                  95

aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta  336
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
             100             105                 110

gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt  384
Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
```

196

```
tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att     432
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
    130                 135                 140

tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt     480
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
145                 150                 155                 160

aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac     528
Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
                165                 170                 175

ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata     576
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
                180                 185                 190

ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt     624
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
            195                 200                 205

aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga     672
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly
    210                 215                 220

aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt     720
Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
225                 230                 235                 240

att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa     768
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
                245                 250                 255

cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga     816
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg
                260                 265                 270

ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc     864
Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
                275                 280                 285

ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta          908
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
    290                 295                 300
```

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<210> 107
<211> 302
<212> PRT
<213> Pasteurella multocida

<400> 107
Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
  1               5                  10                  15


Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
                20                  25                  30


Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
                35                  40                  45
```

```
Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
    50                  55                  60

Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
65                  70                  75                  80

Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
                85                  90                  95

Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
            100                 105                 110

Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
        115                 120                 125

Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
    130                 135                 140

Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
145                 150                 155                 160

Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
                165                 170                 175

Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
                180                 185                 190

Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
            195                 200                 205

Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly
    210                 215                 220

Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
225                 230                 235                 240

Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
                245                 250                 255

His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg
                260                 265                 270

Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
                275                 280                 285

Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
    290                 295                 300
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<210> 108
<211> 2054
<212> DNA
<213> Pasteurella multocida

<220>
<223> pnp

<220>
<221> CDS
<222> (1)..(2052)

<400> 108
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atg gca agt atg gat gat act act gtg ttt gtc aca gtg gtt gcc aaa      48
Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys
 1               5                  10                  15

aaa gat gtg aaa gaa ggt caa gac ttc ttc cca tta act gtt aac tat      96
Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr
            20                  25                  30

caa gag cgt act tat gct gca ggc cgt att cct ggt ggc ttt ttc aaa     144
Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys
        35                  40                  45

cgt gaa ggt cgt cct tct gaa ggc gaa act tta att gct cgt tta att     192
Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile
        50                  55                  60

gac cgt cca att cgt cct ctt ttc cca gaa ggt ttt tat aac gaa atc     240
Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile
 65                  70                  75                  80

caa atc gtg gcg aca gtg gtg tct gtt aat ccg caa att tgt cca gat     288
Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp
                85                  90                  95

tta gtg gca atg atc ggt gca tct gcg gca ctt tct tta tca ggt gtg     336
Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val
                100                 105                 110

cca ttt aat ggc cct atc ggt gcg gca cgt gtt ggt ttt att gat gat     384
Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp
            115                 120                 125

caa ttt gtg tta aac cca acc atg aac gag caa aaa caa agc cgt tta     432
Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu
    130                 135                 140

gac ttg gtt gtc gcg gga aca gat aaa gcg gtg tta atg gtg gaa tct     480
Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser
145                 150                 155                 160

gaa gcc gat gta tta acc gaa gaa caa atg tta gct gcg gtg gtg ttt     528
Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe
                165                 170                 175

ggt cat cag caa caa caa gtg gtg att gac gcg atc aaa gaa ttt acc     576
Gly His Gln Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr
            180                 185                 190

gca gaa gcc ggt aaa ccg cgt tgg gat tgg gtg gca cct gaa cca aat     624
Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn
        195                 200                 205

acc gcg tta att gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc     672
Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly
        210                 215                 220

gaa gca tac cgt atc act gaa aaa caa gca cgt tat gaa caa att gat     720
Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp
225                 230                 235                 240

gcg att aaa gct gat gtg att gca caa atc aca gct gaa gta gca gaa     768
Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu
```

199

```
ggc gaa gac atc agt gaa ggg aaa att gtc gat att ttc acc gca ctt    816
Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu
            260                 265                 270

gaa agc caa atc gta cgt agc cgt atc att gct ggt gaa cca cgt att    864
Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile
            275                 280                 285

gat ggt cgt aca gtg gat act gtt cgt gca tta gat att tgt act ggt    912
Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly
    290                 295                 300

gtt tta cca cgt aca cac ggt tct gcg att ttc acc cgt ggt gaa aca    960
Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr
305                 310                 315                 320

cag gcg tta gct gtc gcg aca tta ggt aca gaa cgt gat gca caa att   1008
Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile
                325                 330                 335

att gat gaa tta aca ggt gag cgt tca gat cac ttc tta ttc cac tac   1056
Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr
            340                 345                 350

aac ttc ccg cca tat tct gtg ggt gaa acc ggt atg att ggt tca cca   1104
Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro
            355                 360                 365

aaa cgt cgt gaa att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct   1152
Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala
    370                 375                 380

gca gtg atg cca aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc   1200
Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val
385                 390                 395                 400

tct gaa atc aca gaa tca aat ggt tct tct tct atg gca tcg gtt tgt   1248
Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys
                405                 410                 415

ggt gcg tct tta gca tta atg gat gcg ggt gta cca att aaa gcg gcg   1296
Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala
            420                 425                 430

gtt gca ggt att gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg   1344
Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val
            435                 440                 445

gtg ctt tca gac atc tta ggt gat gaa gat cac tta ggt gac atg gac   1392
Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp
    450                 455                 460

ttc aaa gtc gcg ggt aca cgt acg ggt gtg acg gca tta caa atg gat   1440
Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp
465                 470                 475                 480

atc aaa atc gaa ggt atc aca gca gaa atc atg caa att gcg tta aac   1488
Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn
                485                 490                 495
```

200

```
caa gcg aaa agc gca cgt tta cac att tta ggt gtg atg gag caa gcg    1536
Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala
            500                 505                 510

atc cca gcg cca cgt gcg gat att tct gat ttt gca ccg cgt att tac    1584
Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr
            515                 520                 525

act atg aaa att gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt    1632
Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly
        530                 535                 540

ggt gca acc att cgt gcc tta aca gaa gaa aca ggt acc tca att gat    1680
Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp
545                 550                 555                 560

atc gat gat gat ggt acg gtg aag att gct gcg gtt gat ggc aat tca    1728
Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser
                565                 570                 575

gca aaa gag gtg atg gcg cgt att gaa gat att act gca gaa gtt gaa    1776
Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu
                580                 585                 590

gcg ggt gca gtg tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt    1824
Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly
            595                 600                 605

gcc ttc gtt tct atc gta ggt aac aaa gaa ggc tta gtg cat att tct    1872
Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser
        610                 615                 620

caa atc gcg gaa gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg    1920
Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val
625                 630                 635                 640

ggg caa gaa gtg act gtt aaa gtg gtt gag att gat cgt caa ggt cgt    1968
Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg
                645                 650                 655

att cgt tta acc atg aaa gaa gtt gca cca aag caa gaa cac gtt gat    2016
Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp
                660                 665                 670

tct gtt gtc gca gac gtt gcc gca gaa gaa aac gca ta                 2054
Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala
            675                 680


<210> 109
<211> 684
<212> PRT
<213> Pasteurella multocida

<400> 109
Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys
  1               5                 10                  15


Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr
            20                  25                  30


Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys
```

201

Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile
    50   55   60

Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile
65   70   75   80

Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp
            85   90   95

Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val
           100   105   110

Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp
       115   120   125

Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu
       130   135   140

Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser
145   150   155   160

Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe
           165   170   175

Gly His Gln Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr
       180   185   190

Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn
       195   200   205

Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly
     210   215   220

Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp
225   230   235   240

Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu
           245   250   255

Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu
       260   265   270

Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile
       275   280   285

Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly
     290   295   300

Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr
305   310   315   320

Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile
           325   330   335

Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr
       340   345   350

Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro
       355   360   365

```
Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala
    370             375             380

Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val
385             390             395             400

Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys
                405             410             415

Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala
            420             425             430

Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val
            435             440             445

Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp
    450             455             460

Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp
465             470             475             480

Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn
                485             490             495

Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala
            500             505             510

Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr
            515             520             525

Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly
    530             535             540

Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp
545             550             555             560

Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser
            565             570             575

Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu
            580             585             590

Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly
    595             600             605

Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser
    610             615             620

Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val
625             630             635             640

Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg
            645             650             655

Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp
            660             665             670

Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala
    675             680
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<210> 110

203

<211> 1514
<212> DNA
<213> Pasteurella multocida

<220>
<223> purF

<220>
<221> CDS
<222> (1)..(1512)

<400> 110
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atg tgt ggt att gtt ggt att gtt agc caa agc ccc gtt aac caa tca      48
Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser
 1               5                  10                  15

att tat gat gcg tta acc tta ttg caa cac cgc ggg caa gac gcc gcc      96
Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
            20                  25                  30

ggg att gta acc gta gat gat gaa aac cga ttc cgc ttg cgt aaa gcg     144
Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
        35                  40                  45

aac ggg tta gtc agc gat gta ttt gaa caa gtt cat atg tta cgt tta     192
Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu
    50                  55                  60

caa ggc aat gct ggc att gga cat gtt cgt tat cct acg gct ggg agc     240
Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
 65                  70                  75                  80

tca agt gtc tct gaa gcg caa cct ttt tat gta aat tcg cct tat ggc     288
Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
                85                  90                  95

tta acc tta gtg cat aat ggt aac ttg acc aat tca agt gaa tta aaa     336
Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
            100                 105                 110

gaa aag tta ttt cgt ctc gca cgt cgc cat gta aat acc aat tca gat     384
Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
        115                 120                 125

tct gaa tta tta ctc aat atc tta gcc aat cac ctt gat cac ttc gaa     432
Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
    130                 135                 140

aaa tac caa tta gat ccg caa gat gta ttc agt gct gtc aaa caa acg     480
Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
145                 150                 155                 160

cat cag gat att cgt ggt gct tat gct tgt atc gcc atg att att ggt     528
His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
                165                 170                 175

cat ggt atg gtc gcg ttt cgt gat ccg aac ggt atc cgt ccg tta gtg     576
His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
            180                 185                 190

tta ggg aaa cgc gag gaa aat ggc aaa aca gag tat atg ttt gcc tcc     624
Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser
```

204

```
gaa agt atc gca tta gat aca gtg ggt ttt gag ttt gta cga gat gta    672
Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val
    210             215                 220

caa ccc ggc gaa gcg att tat gtc acg ttt gaa ggg gaa atg tat gct    720
Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala
225                 230                 235                 240

cag caa tgc gca gac aaa cca aca tta aca cct tgt att ttt gaa tac    768
Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr
                245                 250                 255

gtc tat ttt gca cgt cca gac tct tgc atc gat ggg gtt tct gtt tat    816
Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr
                260                 265                 270

gct gcc cgt gtt cat atg gga caa cgt tta ggt gaa aaa att gca cgg    864
Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg
                275                 280                 285

gaa tgg gcg gat gtg gat gat att gat gtg gtc att cct gtg cct gaa    912
Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu
    290                 295                 300

acc tct aac gat att gct tta cgt att gcg cgc gtg tta aat aaa ccg    960
Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro
305                 310                 315                 320

tat cgt caa ggt ttt gtg aaa aat cgc tat gta gga cgt acg ttt att   1008
Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile
                325                 330                 335

atg ccg ggg cag gca ttg cga gtc agt tct gtt aga cgt aaa ctc aat   1056
Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn
                340                 345                 350

acc att gct tca gaa ttt aaa gat aag aat gtg tta tta gtt gac gac   1104
Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp
                355                 360                 365

tcg att gta cgt ggt acc acg tct gaa caa att gtc gaa atg gcg aga   1152
Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg
    370                 375                 380

gcg gca ggt gcg aag aaa att tat ttt gcc tct gct gca cca gaa att   1200
Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile
385                 390                 395                 400

cgt tat cca aat gtg tat ggt att gat atg cca acc aaa aat gaa ttg   1248
Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu
                405                 410                 415

atc gct tat ggt cgt gat gta gat gaa att gct aac tta att ggt gtg   1296
Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val
                420                 425                 430

gat aaa ttg att ttc caa gat ttg gat gcg tta act ggt tct gtg caa   1344
Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln
                435                 440                 445
```

205

```
caa gaa aat cca agt att caa gac ttt gat tgt tcg gtg ttt aca ggg    1392
Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly
    450             455             460

gtt tat gtg acg ggc gat att aca cct gaa tat ctg gat aat att gca    1440
Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala
465             470             475             480

gaa cag cgt aat gat atc gcc aag aaa aag cgt gaa aaa gat gct acc    1488
Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr
            485             490             495

aat ctt gaa atg cac aat gaa aaa ta                                 1514
Asn Leu Glu Met His Asn Glu Lys
            500
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<210> 111
<211> 504
<212> PRT
<213> Pasteurella multocida

<400> 111

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Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser
1               5               10                  15

Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
            20              25                  30

Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
            35              40                  45

Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu
        50              55                  60

Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
65                  70              75                  80

Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
                85              90                  95

Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
            100             105                 110

Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
            115             120                 125

Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
    130             135                 140

Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
145             150                 155                 160

His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
                165                 170                 175

His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
            180                 185                 190

Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser
            195                 200                 205
```

206

```
Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val
    210                 215             220

Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala
225                 230             235                     240

Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr
                245             250                     255

Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr
                260             265             270

Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg
            275             280             285

Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu
        290             295             300

Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro
305                 310             315                     320

Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile
                325                 330             335

Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn
            340             345             350

Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp
            355             360             365

Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg
    370             375             380

Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile
385             390             395                     400

Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu
                405             410             415

Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val
            420             425             430

Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln
        435             440             445

Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly
    450             455             460

Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala
465             470             475                     480

Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr
            485             490             495

Asn Leu Glu Met His Asn Glu Lys
        500


<210> 112
<211> 989
<212> DNA
<213> Pasteurella multocida


207
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<220>
<223> rci

<220>
<221> CDS
<222> (1)..(987)

<400> 112
atg gca aca ata aga aaa cgt ggt aac tca tat cgt gct gag ata agc   48
Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser
 1   5   10   15

aaa aac gga gta agg aaa tca gca aca ttt aag act aaa tca gaa gct   96
Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala
             20   25   30

aat gcg tgg gct gtt gac gag gag aga aaa tta gct gat ttg gca aaa   144
Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys
         35   40   45

ggt atc gct cca gat att att ttt aga gat gta ata gaa cgc tat caa   192
Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln
     50   55   60

aat gaa gtg tct ata act aaa aaa ggc gcg cga aat gaa att ata aga   240
Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg
 65   70   75   80

tta aac cgc ttt tta aga tat gat att tct aat ctg tat att cgt gat   288
Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp
                 85   90   95

tta aga aaa gaa gat ttt gag gag tgg atc aga att cgc cta acc gaa   336
Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu
             100   105   110

gta tcg gat gct agc gtt aga cgt gag ctt gtt act ata tcg tca gtg   384
Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val
         115   120   125

ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg   432
Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met
     130   135   140

act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat   480
Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr
145   150   155   160

tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa   528
Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu
                 165   170   175

gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta   576
Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu
             180   185   190

ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa   624
Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys
         195   200   205

tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act   672
Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr

208

```
aaa aac ggg cac tct aga gat gtg ccg ctt tcg caa aga gct gtt gcg   720
Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala
225             230             235             240

cta att tta aaa atg aaa gag gta gaa aat gga gat ctt gtg ttt cag   768
Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln
                245             250             255

acc acg cct gaa tca tta agc acc acg ttt aga gtg tta aag aaa gag   816
Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu
            260             265             270

tgt gga ctt gaa cat ctc cat ttt cat gat acg aga agg gaa gcg ttg   864
Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu
            275             280             285

acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc   912
Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser
        290             295             300

gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat   960
Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn
305             310             315             320

atg agt gaa gtg gca aac ttg ttg gat ta                           989
Met Ser Glu Val Ala Asn Leu Leu Asp
            325
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<210> 113
<211> 329
<212> PRT
<213> Pasteurella multocida

<400> 113

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Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser
 1               5                  10                  15

Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala
            20                  25                  30

Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys
            35                  40                  45

Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln
    50                  55                  60

Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg
65                  70                  75                  80

Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp
                85                  90                  95

Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu
                100                 105                 110

Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val
            115                 120                 125

Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met
```

Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr
145   150   155   160

Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu
                    165   170   175

Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu
                    180   185   190

Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys
                    195   200   205

Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr
210   215   220

Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala
225   230   235   240

Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln
                    245   250   255

Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu
                    260   265   270

Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu
                    275   280   285

Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser
                    290   295   300

Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn
305   310   315   320

Met Ser Glu Val Ala Asn Leu Leu Asp
                    325

<210> 114
<211> 1190
<212> DNA
<213> Pasteurella multocida

<220>
<223> sopE

<220>
<221> CDS
<222> (1)..(1188)

<400> 114
atg tct gaa gaa tat cta cat ggt gtc aaa gtc aca gaa atc aat caa   48
Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln
 1   5   10   15

gca att cgc aca att caa agt cta tca acc gca gtc atc ggt att gtc   96
Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val
                20   25   30

tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat gaa ccc   144
Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro

```
gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga aaa caa    192
Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln
     50                  55                  60

ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc aat tgc    240
Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys
 65                  70                  75                  80

aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac gaa gaa    288
Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu
                 85                  90                  95

aca aaa gca agt gaa atg aac acg gca att att ggc aca atc aca gaa    336
Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu
                 100                 105                 110

gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa aac aaa    384
Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys
                 115                 120                 125

ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac aca aaa    432
Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys
         130                 135                 140

gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac gca ttt    480
Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe
145                 150                 155                 160

gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg gtg caa    528
Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln
                 165                 170                 175

tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg ggc gat    576
Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp
                 180                 185                 190

ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac tat gcc    624
Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala
         195                 200                 205

gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa cag ggc    672
Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly
     210                 215                 220

tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc ggt gtc    720
Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val
225                 230                 235                 240

aca caa cca ctc tat ttt gac att aac gac agc tcg act gat gtg aac    768
Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn
                 245                 250                 255

tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat ggc ttt    816
Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe
                 260                 265                 270

cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc aag ttt    864
Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe
         275                 280                 285
```

211

```
gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg    912
Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly
    290             295             300

gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta gtg aaa    960
Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys
305             310             315             320

gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc aca aaa   1008
Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys
            325             330             335

ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt aac agt   1056
Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser
        340             345             350

gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat tat cac   1104
Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His
        355             360             365

cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att tct gat   1152
Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp
        370             375             380

gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg ta                1190
Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385             390             395


<210> 115
<211> 396
<212> PRT
<213> Pasteurella multocida

<400> 115
Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln
 1               5              10                  15

Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val
            20              25              30

Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro
            35              40              45

Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln
        50              55              60

Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys
65              70              75              80

Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu
            85              90              95

Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu
            100             105             110

Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys
        115             120             125

Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys
        130             135             140
```

212

```
Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe
145             150             155                 160

Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln
                165             170             175

Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp
            180             185                 190

Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala
            195             200             205

Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly
        210             215             220

Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val
225             230             235                 240

Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn
            245             250             255

Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe
            260             265             270

Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe
        275             280             285

Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly
    290             295             300

Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys
305             310             315                 320

Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys
            325             330             335

Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser
            340             345             350

Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His
            355             360             365

Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp
370             375             380

Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385             390             395


<210> 116
<211> 2204
<212> DNA
<213> Pasteurella multocida

<220>
<223> unkK

<220>
<221> CDS
<222> (1)..(2202)

<400> 116
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213

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atg aat aaa aat cgc tat aaa ctc att ttt agt aaa act aaa ggc tgt     48
Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys
 1               5                  10                  15

ctt gta cct gtt gct gaa acg att aat tct gca gta gga aat gcc tca     96
Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser
                20                  25                  30

tca aaa gac gtt tct gac acc gag ata agt gct tct caa cca gcg ctc    144
Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu
            35                  40                  45

aac tcg ccg ctt tcg acc ctt tct gta tta gtc aaa acc gca ttt aat    192
Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn
        50                  55                  60

ccg gtt tca aca ttg atg tcg ttg act tgg aaa gaa tac gcc gtt tta    240
Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu
65                  70                  75                  80

tta tta agt gtg gtg tct ttt cct ctt atg gca caa gcc tct gat aca    288
Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr
                85                  90                  95

gat tca gtg gta caa aga aaa cct gaa tta act gat gtg acg aat agc    336
Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser
            100                 105                 110

aac agc tat cat gtg gaa tta gat aga gag cat cat aaa ggg gag cat    384
Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His
        115                 120                 125

caa aca aaa atc aaa cat act gag aat aat gtc atc att gtt gat att    432
Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile
    130                 135                 140

gca aaa cca aac caa aag ggc att tca gat aac cgt ttt aaa cac ttc    480
Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe
145                 150                 155                 160

aac atc cca aat ggg gcg gta ttt aac aat agc gcc aag gaa aaa cgc    528
Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg
                165                 170                 175

tca cag tta gtg ggg tat ttg cca ggt aac cag aat tta acg gaa ggt    576
Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly
                180                 185                 190

agt gaa gca aaa gcg atc tta aat cag gtg act gga ccg gat gcc agt    624
Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser
            195                 200                 205

aaa att gaa ggc gcc ctt gaa att tta ggg caa aaa gcc gat ttg gtg    672
Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val
            210                 215                 220

att gcg aac caa aat ggc att gtg ctt aat ggg gta aaa acc att aat    720
Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn
225                 230                 235                 240

gcc aat cgt ttt gtg gca aca acc agt agt acc att gat cct gag caa    768
Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln
```

214

```
atg cag tta aat gtc acg caa ggt aca gtg aca att ggg gtg gat gga    816
Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly
        260             265             270

ttt gcc aca gat ggc tta cct tat ttg gat atc att gcc aaa aag att    864
Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile
        275             280             285

gaa caa aaa caa gcg att aca aaa gaa aga aca gga aat tcc gaa acc    912
Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr
        290             295             300

gat atc act ttt gtc gca ggt aac agt aaa tat gat tta aag aca cat    960
Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His
305                 310             315                 320

caa gtg aca gaa aag cat acc gct gag gca caa ggt gaa att gcg att   1008
Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile
                325             330             335

agc ggt gcg agt acc ggt gca atg tac ggt aaa aat atc aaa tta atc   1056
Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile
                340             345             350

gta acg gat aaa ggc gct ggg gta aaa cat gat ggc att att tta tct   1104
Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser
            355             360             365

gag gcg gat att caa att gaa acc cat gag ggc gat gtt gaa tta ggc   1152
Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly
        370             375             380

aat aca aaa aat aat cag aat gag aat tat gcc aaa gct cat gcg gaa   1200
Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu
385                 390             395                 400

ggg aat ttt acg gtt aaa ggc ggt aag cac gtt att att ggt aag gaa   1248
Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu
                405             410             415

gtt aaa gcc aac aaa gcg gtc gat att caa gca caa gaa aca aca gta   1296
Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val
                420             425             430

aga caa aat gcg aaa tta act gcc aaa acg agt gcc aaa att aca gca   1344
Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala
        435             440             445

agt aag agt gtg aat ctt gaa gat aac gcg aaa ctt att gct aat gag   1392
Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu
        450             455             460

ctg agc aca aca acc aat aaa tta acc aat aaa ggt agc att tac ggc   1440
Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly
465                 470             475                 480

aag aaa gtg acg cta gat gct gat aat tta gtc aat agt aaa gaa atc   1488
Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile
                485             490             495
```

215

```
tat gcg tct agc gaa ctt gat att caa acc aaa ggt cgt gat ctt tta       1536
Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu
            500                     505                 510

ctt gag gat ggg gtt aat caa cca ctg agt ttc tta aaa ggc gct tca       1584
Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser
            515                     520                 525

ttg tta gcg ccg ggg ttt gtc aac act ggg cta att cac agt aac ggt       1632
Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly
        530                     535                 540

aat gcc aag ctc act ttt aaa gat gac acc agt ttt gtg act gaa gga       1680
Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly
545                     550                     555                 560

aat aac ttt atc aca gca aaa gac aac tta gaa atc acg gca aaa aat       1728
Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn
                565                     570                 575

gtt caa att gat caa gcg aaa aat att caa tta aac gcg aat atc acg       1776
Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr
            580                     585                 590

atc aat acc aag tct ggt ttt gtg aat tac ggt acc tta gca agt gct       1824
Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala
            595                     600                 605

caa aat tta acg att aat acc gaa caa ggc agc att tat aac ata ggc       1872
Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly
        610                     615                 620

ggt atc ttg ggg gcg ggt aaa agt ttg aat ctg agc gcg aaa aga gga       1920
Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly
625                     630                     635                 640

gaa aac caa gga gga tat ctt att aat caa ggt aag agt cta ctc cat       1968
Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His
                645                     650                 655

tct gaa ggc gcc atg aac ctc aca gcg gat cgc acg gtg tac aat tta       2016
Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu
            660                     665                 670

ggg aat att ttt gct aaa ggt gac gcg acg atc aat gca aac gcg tta       2064
Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu
            675                     680                 685

att aat gat gtt act ctc aca ggt cgt ctt gag tat caa gat ctg aaa       2112
Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys
        690                     695                 700

aaa gat tat acg cgt tat tat cgt atc aat gaa acg gca aaa cat ggt       2160
Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly
705                     710                     715                 720

tgg cat aat aac ttc tat gaa tta aac gtc gac aga gtt tct tg            2204
Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser
                725                     730
```

<210> 117

216

<211> 734
<212> PRT
<213> Pasteurella multocida

<400> 117
Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys
1   5   10   15

Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser
            20   25   30

Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu
        35   40   45

Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn
    50   55   60

Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu
65   70   75   80

Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr
            85   90   95

Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser
            100   105   110

Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His
        115   120   125

Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile
    130   135   140

Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe
145   150   155   160

Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg
            165   170   175

Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly
        180   185   190

Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser
    195   200   205

Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val
    210   215   220

Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn
225   230   235   240

Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln
            245   250   255

Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly
        260   265   270

Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile
        275   280   285

Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr
    290   295   300

217

```
Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His
305             310             315             320

Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile
                325             330             335

Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile
            340             345             350

Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser
        355             360             365

Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly
    370             375             380

Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu
385             390             395             400

Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu
            405             410             415

Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val
        420             425             430

Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala
        435             440             445

Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu
    450             455             460

Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly
465             470             475             480

Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile
            485             490             495

Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu
        500             505             510

Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser
        515             520             525

Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly
    530             535             540

Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly
545             550             555             560

Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn
            565             570             575

Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr
        580             585             590

Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala
        595             600             605

Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly
    610             615             620

Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly
625             630             635             640
```

218

```
Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His
                645                 650             655

Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu
            660             665             670

Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu
        675             680             685

Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys
    690             695             700

Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly
705             710             715                 720

Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser
                725             730
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<210> 118
<211> 251
<212> DNA
<213> Pasteurella multocida

<220>
<223> unk0

<220>
<221> CDS
<222> (1)..(249)

<400> 118
```
atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc    48
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
  1               5                  10                  15

gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca    96
Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
            20                  25                  30

tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt   144
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
            35                  40                  45

gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga   192
Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
        50                  55                  60

agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat   240
Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
    65                  70                  75                  80

tgt aat cat ta                                                     251
Cys Asn His
```

<210> 119
<211> 83
<212> PRT
<213> Pasteurella multocida

<400> 119

219

```
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
1               5                   10                  15

Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
            20                  25                  30

Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
        35                  40                  45

Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
    50                  55                  60

Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
65                  70                  75                  80

Cys Asn His
```

<210> 120
<211> 548
<212> DNA
<213> Pasteurella multocida

<220>
<223> unkP

<220>
<221> CDS
<222> (1)..(546)

<400> 120
```
atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att tca     48
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
1               5                   10                  15

aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat ttt     96
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
            20                  25                  30

gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa ggc    144
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
            35                  40                  45

atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta cgc    192
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
        50                  55                  60

acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc act    240
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65                  70                  75                  80

gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca gtg    288
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
                85                  90                  95

gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca atc    336
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
                100                 105                 110

aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc ggt    384
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
```

220

```
aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat   432
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
    130                 135                 140

gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa   480
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145             150                 155                 160

cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt   528
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
                165                 170                 175

tca aat cgt tta gca tcg ta                                        548
Ser Asn Arg Leu Ala Ser
            180
```

<210> 121
<211> 182
<212> PRT
<213> Pasteurella multocida

<400> 121

```
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
 1               5                   10                  15

Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
            20                  25                  30

Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
        35                  40                  45

Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
    50                  55                  60

Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65                  70                  75                  80

Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
                85                  90                  95

Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
            100                 105                 110

Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
            115                 120                 125

Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
    130                 135                 140

Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145             150                 155                 160

Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
                165                 170                 175

Ser Asn Arg Leu Ala Ser
            180
```

<210> 122
<211> 69
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> apvA-or1

<220>
<221> CDS
<222> (1)..(69)

<400> 122
```
atg ttt tat gtc atg ctt gcc aat agg acg tct ata att tca tca atc      48
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
  1               5                   10                  15

gat aag ttt aag ata ctt agc                                          69
Asp Lys Phe Lys Ile Leu Ser
             20
```

<210> 123
<211> 23
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 123
```
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
  1               5                   10                  15

Asp Lys Phe Lys Ile Leu Ser
             20
```

<210> 124
<211> 64
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> apvA-or2

<220>
<221> CDS
<222> (3)..(62)

<400> 124
```
ag cta agt atc tta aac tta tcg att gat gaa att ata gac gtc cta       47
   Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu
     1               5                   10                  15

ttg gca agc atg aca ta                                               64
Leu Ala Ser Met Thr
             20
```

<210> 125
<211> 20
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 125
Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu Leu
 1   5   10   15

Ala Ser Met Thr
             20

<210> 126
<211> 653
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> apvB

<220>
<221> CDS
<222> (1)..(651)

<400> 126
tta att agc ttt cct ttt att act ttt gca agt aat gtt aat gga gcc   48
Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1   5   10   15

gaa att gga ttg gga gga gcc cgt gag agt agt att tac tat tct aaa   96
Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
             20   25   30

cat aaa gta gca aca aat ccc ttt tta gca ctt gat ctt tct tta ggt   144
His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
         35   40   45

aat ttt tat atg aga ggg act gca gga att agc gaa ata gga tat gaa   192
Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
     50   55   60

caa tct ttc act gac aat ttc agc gta tca ctg ttt gtt aac cca ttt   240
Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
 65   70   75   80

gat ggt ttt tca att aaa gga aaa gac ttg tta cct gga tat caa agt   288
Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
                 85   90   95

att caa act cgc aaa act caa ttt gcc ttt ggt tgg gga tta aat tat   336
Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
                100   105   110

aat ttg gga ggt tta ttc ggc tta aat gat act ttt ata tcc ttg gaa   384
Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
             115   120   125

gga aaa agc gga aaa cgt ggt gcg agt agt aat gtc agc tta ctt aaa   432
Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
         130   135   140

tcg ttt aat atg acg aaa aat tgg aaa gtt tca cca tat att ggc tca   480
Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
145   150   155   160

agt tat tat tca tct aaa tat aca gat tat tac ttt ggt att aaa caa   528

223

```
Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
                 165             170                 175

tcc gaa tta ggt aat aaa att aca tcc gta tat aaa cct aaa gca gct   576
Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
                 180             185                 190

tat gca aca cac ata ggt att aat act gat tat gct ttc acg aac aat   624
Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
                 195             200                 205

ctt ggc atg ggt tta tct gtc ggt tgg at                            653
Leu Gly Met Gly Leu Ser Val Gly Trp
                 210             215
```

<210> 127
<211> 217
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 127
```
Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1               5                   10                  15

Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
                 20              25                  30

His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
                 35              40                  45

Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
         50              55                  60

Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
 65                  70                  75                  80

Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
                 85                  90                  95

Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
                 100             105                 110

Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
         115                 120                 125

Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
 130                 135                 140

Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
145                 150                 155                 160

Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
                 165             170                 175

Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
                 180             185                 190

Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
                 195             200                 205

Leu Gly Met Gly Leu Ser Val Gly Trp
```

224

<210> 128
<211> 242
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> apvC

<220>
<221> CDS
<222> (1)..(240)

<400> 128
atg tgg cgg atg gga gat ttt atg tct aaa aaa gag agg ctg aat gat   48
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1   5   10   15

atg gct cgc cag att tta tca gcg gcg gag ttg ctc att gca aag gaa   96
Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
                20   25   30

ggt ttg caa aat tta tcg atg agg aaa atc gca agt gaa gcc ggt atc   144
Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
            35   40   45

gca aca ggc acg ctt tat ctc tat ttc aaa acg aaa gac gag tta ctg   192
Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
        50   55   60

gat tgt ttg gcg gaa caa tta cat gaa cga tat tat cgt tat ctg aat   240
Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
65   70   75   80

at   242

<210> 129
<211> 80
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 129
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1   5   10   15

Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
                20   25   30

Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
            35   40   45

Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
        50   55   60

Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
65   70   75   80

<210> 130

<400> 130

```
aat att caa aaa aca gtt att gct agc ggc aca ttg caa gcg act gaa    48
Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
 1               5                  10                  15

caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta    96
Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
            20                  25                  30

gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att   144
Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
        35                  40                  45

gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta   192
Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
    50                  55                  60

gca aat gct tct gct aat ttg gat aca aaa aaa att aat ctt aag caa   240
Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
65                  70                  75                  80

ctg caa tca gat tgg gaa cgt cat caa cgt ttg ata cga acc aat gcg   288
Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
                85                  90                  95

aca agc caa aag gaa aca gaa gaa gca aaa agt aga tta aat acg gcc   336
Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
            100                 105                 110

aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc   384
Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
            115                 120                 125

aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct   432
Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
    130                 135                 140

cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act   480
Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
145                 150                 155                 160

tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at    527
Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
            165                 170                 175
```

<400> 131
Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
1   5   10   15

Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
                20   25   30

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
            35   40   45

Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
        50   55   60

Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
65   70   75   80

Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
                85   90   95

Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
                100   105   110

Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
            115   120   125

Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
        130   135   140

Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
145   150   155   160

Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
                165   170   175

<210> 132
<211> 867
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> atpG

<220>
<221> CDS
<222> (1)..(864)

<400> 132
atg gca ggt gcg aaa gag ata aga acc aaa att gca agt gtg aaa aat   48
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn
1   5   10   15

act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg   96
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met
                20   25   30

cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tcg gaa aca   144
Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr
                35   40   45

atc cgt aag gtg att agc cat att gcg aaa gga agc att ggt tat aag   192
Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys

227

```
              50                           55                           60
cac  ccg  ttt  tta  act  gaa  cgt  gat  att  aaa  aaa  gta  ggc  tat  ctt  gtc    240
His  Pro  Phe  Leu  Thr  Glu  Arg  Asp  Ile  Lys  Lys  Val  Gly  Tyr  Leu  Val
 65                           70                      75                      80

gtt  tcg  acc  gat  cgc  ggt  tta  tgc  ggt  ggc  ctt  aat  atc  aat  tta  ttc    288
Val  Ser  Thr  Asp  Arg  Gly  Leu  Cys  Gly  Gly  Leu  Asn  Ile  Asn  Leu  Phe
                    85                      90                      95

aaa  gcg  act  ttg  aat  gaa  ttt  aaa  acg  tgg  aaa  gat  aaa  gac  gtt  agt    336
Lys  Ala  Thr  Leu  Asn  Glu  Phe  Lys  Thr  Trp  Lys  Asp  Lys  Asp  Val  Ser
               100                      105                      110

gtt  gag  ctt  ggt  tta  gta  ggg  tcg  aaa  ggc  gta  agc  ttt  tac  caa  aat    384
Val  Glu  Leu  Gly  Leu  Val  Gly  Ser  Lys  Gly  Val  Ser  Phe  Tyr  Gln  Asn
               115                      120                      125

cta  ggc  tta  aac  gtg  aga  tct  caa  gta  acg  gga  tta  ggc  gat  aat  ccg    432
Leu  Gly  Leu  Asn  Val  Arg  Ser  Gln  Val  Thr  Gly  Leu  Gly  Asp  Asn  Pro
          130                      135                      140

gaa  atg  gaa  cgt  atc  gtg  ggc  gca·gtt  aat  gaa  atg  att  aat  gcg  ttc    480
Glu  Met  Glu  Arg  Ile  Val  Gly  Ala  Val  Asn  Glu  Met  Ile  Asn  Ala  Phe
145                      150                      155                      160

cga  aac  gga  gaa  gtg  gat  gcg  gtt  tac  gtc  gct  tac  aac  cgt  ttt  gaa    528
Arg  Asn  Gly  Glu  Val  Asp  Ala  Val  Tyr  Val  Ala  Tyr  Asn  Arg  Phe  Glu
                    165                      170                      175

aat  acg  atg  tca  caa  aaa  cct  gtt  atc  gca  cag  tta  ctt  ccg  tta  cct    576
Asn  Thr  Met  Ser  Gln  Lys  Pro  Val  Ile  Ala  Gln  Leu  Leu  Pro  Leu  Pro
               180                      185                      190

aaa  cta  gat  gac  gat  gaa  tta  gat  acg  aaa  ggt  tca  tgg  gat  tat  att    624
Lys  Leu  Asp  Asp  Asp  Glu  Leu  Asp  Thr  Lys  Gly  Ser  Trp  Asp  Tyr  Ile
               195                      200                      205

tat  gaa  ccg  aat  cca  caa  gtt  tta  ttg  gat  agt  tta  ctt  gtt  cgt  tat    672
Tyr  Glu  Pro  Asn  Pro  Gln  Val  Leu  Leu  Asp  Ser  Leu  Leu  Val  Arg  Tyr
          210                      215                      220

tta  gaa  act  cag  gta  tac  caa  gca  gtt  gta  gat  aac  cta  gct  tct  gaa    720
Leu  Glu  Thr  Gln  Val  Tyr  Gln  Ala  Val  Val  Asp  Asn  Leu  Ala  Ser  Glu
225                      230                      235                      240

caa  gcc  gct  cga  atg  gta  gcg  atg  aaa  gcc  gca  aca  gat  aat  gcg  ggt    768
Gln  Ala  Ala  Arg  Met  Val  Ala  Met  Lys  Ala  Ala  Thr  Asp  Asn  Ala  Gly
                    245                      250                      255

aca  tta  atc  gat  gaa  tta  caa  tta  gtg  tat  aac  aaa  gct  cgc  caa  gca    816
Thr  Leu  Ile  Asp  Glu  Leu  Gln  Leu  Val  Tyr  Asn  Lys  Ala  Arg  Gln  Ala
                    260                      265                      270

agc  att  aca  aat  gaa  tta  aac  gaa  att  gtt  gcg  ggt  gcc  gca  gca  att    864
Ser  Ile  Thr  Asn  Glu  Leu  Asn  Glu  Ile  Val  Ala  Gly  Ala  Ala  Ala  Ile
          275                      280                      285

taa                                                                              867
```

<210> 133

228

<211> 288
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 133
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn
 1   5   10   15

Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met
            20   25   30

Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr
            35   40   45

Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys
        50   55   60

His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val
65   70   75   80

Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
                85   90   95

Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser
            100   105   110

Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn
            115   120   125

Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro
        130   135   140

Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe
145   150   155   160

Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu
                165   170   175

Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro
            180   185   190

Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile
        195   200   205

Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr
210   215   220

Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
225   230   235   240

Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly
            245   250   255

Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
            260   265   270

Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
        275   280   285

<210> 134
<211> 534

229

<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> atpH

<220>
<221> CDS
<222> (1)..(531)

<400> 134
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atg tca gaa tta agt aca gta gct cgc ccc tac gct aaa gca gct ttt      48
Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1               5                  10                  15

gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta      96
Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
                20                  25                  30

cag ttt tcg gca ttc gtt gct gaa aac gaa caa gtg gcg gaa tat att     144
Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
            35                  40                  45

aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc     192
Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
        50                  55                  60

tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg     240
Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
 65                  70                  75                  80

gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc     288
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
                85                  90                  95

gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt     336
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
               100                 105                 110

tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg     384
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
           115                 120                 125

atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat     432
Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
           130                 135                 140

aac agc ctg att gca ggc gta att att aaa tac gat gat gtt gtt att     480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
145                 150                 155                 160

gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc     528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
               165                 170                 175

ttg taa                                                              534
Leu
```

<210> 135
<211> 177
<212> PRT

230

<213> Actinobacillus pleuropneumoniae

<400> 135

```
Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1               5                  10                  15

Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
            20                  25                  30

Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
        35                  40                  45

Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
    50                  55                  60

Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
65                  70                  75                  80

Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
                85                  90                  95

Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
            100                 105                 110

Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
            115                 120                 125

Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
    130                 135                 140

Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
145                 150                 155                 160

Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
                165                 170                 175

Leu
```

<210> 136
<211> 321
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> dksA

<220>
<221> CDS
<222> (1)..(318)

<400> 136
```
gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa    48
Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1               5                  10                  15

atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act    96
Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
            20                  25                  30

cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt   144
```

231

```
Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
        35              40              45

aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac    192
Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
        50              55              60

gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt    240
Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
 65                  70                  75                  80

tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt    288
Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
                85              90              95

gcg gaa atc cgt gaa aag caa atg ggc tta taa                        321
Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
            100             105
```

<210> 137
<211> 106
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 137
```
Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1               5               10                  15

Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
            20              25              30

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
        35              40              45

Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
        50              55              60

Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
 65                  70                  75                  80

Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
                85              90              95

Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
            100             105
```

<210> 138
<211> 33
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> dnaK

<220>
<221> CDS
<222> (1)..(30)

<400> 138
gct gag ttt gaa gaa gtg aaa gat aat aaa taa   33

```
Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
  1               5                   10


<210> 139
<211> 10
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 139
Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
  1               5                   10


<210> 140
<211> 453
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> exbB

<220>
<221> CDS
<222> (1)..(450)

<400> 140
atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att   48
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
  1               5                   10                  15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att   96
Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
              20                  25                  30

gaa cgc gta ctt ttc tac aaa caa ttg gat gtg acc aaa tat gac acg  144
Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
              35                  40                  45

cta caa gat ttg gaa att gat acc act cgc aat tta acc acc att tcc  192
Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
      50                  55                  60

act atc ggt gcc aac gcc cct tat atc ggt tta tta gga acc gta tta  240
Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
 65                  70                  75                  80

ggg atc tta ctt acc ttc tat cat tta ggg cat tcc ggc ggt gat att  288
Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
                  85                  90                  95

gac gcc gca tcc att atg gtt cac ctt tcg ctt gca tta aaa gca acc  336
Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
              100                 105                 110

gca gcc ggt atc tta gtc gct att ccg gca atg atg ttc tac agc ggt  384
Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
          115                 120                 125

ttt aac cgt aaa gtg gat gaa agc aaa ctt aaa tgg caa gcg att caa  432
Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
      130                 135                 140
```

233

```
gct cgt aaa gcc aat caa taa                                    453
Ala Arg Lys Ala Asn Gln
145                 150


<210> 141
<211> 150
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 141
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
1               5                   10                  15

Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
            20                  25                  30

Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
            35                  40                  45

Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
        50                  55                  60

Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
65                  70                  75                  80

Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
                85                  90                  95

Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
                100                 105                 110

Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
            115                 120                 125

Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
        130                 135                 140

Ala Arg Lys Ala Asn Gln
145                 150


<210> 142
<211> 720
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> fkpA

<220>
<221> CDS
<222> (1)..(717)

<400> 142
atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc   48
Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
1               5                   10                  15

gtt tca gct caa act gca ttt gca gcg gat caa aaa ttc att gac gat   96
Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp
            20                  25                  30
```

234

```
tca tca tat gca gtc ggc gta ttg atg ggt aaa aat atc gaa ggc gtc      144
Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val
        35              40                  45

gtt gaa tca caa aaa gaa att ttt tct tat aac caa gat aaa atc ttg      192
Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu
        50              55                  60

gcg ggt gtc caa gat acc atc aaa aaa acc ggt aaa tta acc gat gaa      240
Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu
65                  70                  75                  80

gat cta caa aaa caa tta aaa tcg ctt gat act tat ctt gca agt caa      288
Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln
                85                  90                  95

gaa agc aaa att gcg gcg gag aaa agc aaa gca acc gta gaa gcc ggt      336
Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly
            100                 105                 110

aat aaa ttt cgt acc gac tac gaa aaa caa agc ggc gtg aaa aaa acc      384
Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr
            115                 120                 125

gct tcc ggt tta ctt tat aaa att gaa aaa gcc ggc acg ggc gaa tcg      432
Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser
        130                 135                 140

cct aaa gcg gaa gat acc gtt aaa gtt cac tat aaa ggg aca tta acc      480
Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr
145                 150                 155                 160

gat ggt acg gta ttc gat agc tca tac gat cgc ggt gag ccg att gaa      528
Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu
                165                 170                 175

ttc caa tta aac caa tta att ccg ggt tgg att gaa gcg att cca atg      576
Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met
                180                 185                 190

ttg aaa aaa ggc gga aaa atg gaa atc gtc gtt ccg cct gaa ctt ggt      624
Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
            195                 200                 205

tac ggc gaa cgc caa gca ggt aag att ccg gca agt tca acc tta aaa      672
Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
        210                 215                 220

ttc gag att gaa ttg tta gat ttc aaa gcg gcc gaa gcg aaa aaa taa      720
Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys
225                 230                 235


<210> 143
<211> 239
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 143
Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
 1               5                   10                  15
```

235

```
Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp
            20                  25                  30

Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val
            35                  40                  45

Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu
        50                  55                  60

Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu
65                  70                  75                  80

Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln
                85                  90                  95

Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly
            100                 105                 110

Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr
            115                 120                 125

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser
            130                 135                 140

Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr
145                 150                 155                 160

Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu
                165                 170                 175

Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met
                180                 185                 190

Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
            195                 200                 205

Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
            210                 215                 220

Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys
225                 230                 235


<210> 144
<211> 290
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> HI0379

<220>
<221> CDS
<222> (3)..(287)

<400> 144
tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa     47
   His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln
    1               5                  10                  15

cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat     95
Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn
```

236

```
ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct   143
Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser
            35                  40                  45

cag tgc tta acc cat cat tta tgg gaa cgt tta gaa gaa caa atc ggt   191
Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly
            50                  55                  60

gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg   239
Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser
        65                  70                  75

gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat   287
Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His
80                  85                  90                  95

taa                                                               290
```

<210> 145
<211> 95
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 145
```
His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln Pro
1               5                   10                  15

Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn Leu
                20                  25                  30

Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser Gln
            35                  40                  45

Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly Val
        50                  55                  60

Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser Asp
65                  70                  75                  80

His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His
                85                  90                  95
```

<210> 146
<211> 273
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> hupA

<220>
<221> CDS
<222> (1)..(270)

<400> 146
```
atg aac aaa act gag tta atc gat gca atc gca gct ggt gca gag tta   48
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu
  1               5                   10                  15
```

237

```
agc aag aaa gac gcg aaa gcg gca tta gaa gcg act tta aat gcg atc    96
Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile
            20                  25                  30

tct gaa agc cta aaa aat ggc gac acc gtt cag tta atc ggc ttc ggt   144
Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly
            35                  40                  45

act ttt aaa gta aac gag cgt aat gca cgt acg ggt cgt aac ccg cgt   192
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg
        50                  55                  60

acc ggc gaa gaa atc aaa atc gca gca tct aaa gtg ccg gcg ttt gtt   240
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val
65                  70                  75                  80

gca ggt aaa gca tta aaa gat tta gta aaa taa                       273
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys
                85                  90


<210> 147
<211> 90
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 147
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu
1               5                   10                  15

Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile
            20                  25                  30

Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly
            35                  40                  45

Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg
        50                  55                  60

Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val
65                  70                  75                  80

Ala Gly Lys Ala Leu Lys Asp Leu Val Lys
                85                  90


<210> 148
<211> 551
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> lpdA

<220>
<221> CDS
<222> (1)..(549)

<400> 148
atg agc aaa gaa atc aaa acg caa gtc gtg gta ctt ggt gcg ggt cct   48
Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro
1               5                   10                  15
```

238

```
gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca      96
Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
             20              25              30

gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta     144
Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
         35              40              45

ggt tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa     192
Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
     50              55              60

gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac     240
Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn
65              70              75              80

att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa     288
Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
                 85              90              95

tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta     336
Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
             100             105             110

gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt     384
Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
             115             120             125

gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att     432
Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
     130             135             140

gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat     480
Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
145             150             155             160

ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc     528
Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
             165             170             175

gaa aaa att act cat tat ggg cc                                      551
Glu Lys Ile Thr His Tyr Gly
             180
```

<210> 149
<211> 183
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 149

```
Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro
 1               5              10              15

Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
             20              25              30

Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
         35              40              45

Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
     50              55              60
```

239

```
Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn
 65              70              75              80

Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
                 85              90              95

Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
             100             105             110

Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
             115             120             125

Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
     130             135             140

Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
145             150             155             160

Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
             165             170             175

Glu Lys Ile Thr His Tyr Gly
             180


<210> 150
<211> 1095
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> Omp5-2

<220>
<221> CDS
<222> (1)..(1092)

<400> 150
atg aaa aaa tca tta gtt gct tta aca gta tta tcg gct gca gcg gta    48
Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val
 1           5               10              15

gct caa gca gcg cca caa caa aat act ttc tac gca ggt gcg aaa gca    96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala
             20              25              30

ggt tgg gcg tca ttc cat gat ggt atc gaa caa tta gat tca gct aaa   144
Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys
         35              40              45

aac aca gat cgc ggt aca aaa tac ggt atc aac cgt aat tca gta act   192
Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr
     50              55              60

tac ggc gta ttc ggc ggt tac caa att tta aac caa gac aaa tta ggt   240
Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly
 65              70              75              80

tta gcg gct gaa tta ggt tat gac tat ttc ggt cgt gtg cgc ggt tct   288
Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser
             85              90              95
```

240

```
gaa aaa cca aac ggt aaa gcg gac aag aaa act ttc cgt cac gct gca    336
Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala
            100             105             110

cac ggt gcg aca atc gca tta aaa cct agc tac gaa gta tta cct gac    384
His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp
            115             120             125

tta gac gtt tac ggt aaa gta ggt atc gca tta gta aac aat aca tat    432
Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr
            130             135             140

aaa aca ttc aat gca gca caa gag aaa gtg aaa act cgt cgt ttc caa    480
Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln
145             150             155             160

agt tct tta att tta ggt gcg ggt gtt gag tac gca att ctt cct gaa    528
Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu
                165             170             175

tta gcg gca cgt gtt gaa tac caa tgg tta aac aac gca ggt aaa gca    576
Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala
            180             185             190

agc tac tct act tta aat cgt atg ggt gca act gac tac cgt tcg gat    624
Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp
            195             200             205

atc agt tcc gta tct gca ggt tta agc tac cgt ttc ggt caa ggt gcg    672
Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala
            210             215             220

gca ccg gtt gca gct ccg gca gtt gaa act aaa aac ttc gca ttc agc    720
Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser
225             230             235             240

tct gac gta tta ttc gca ttc ggt aaa tca aac tta aaa ccg gct gcg    768
Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala
                245             250             255

gca aca gca tta gat gca atg caa acc gaa atc aat aac gca ggt tta    816
Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu
            260             265             270

tca aat gct gcg atc caa gta aac ggt tac acg gac cgt atc ggt aaa    864
Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys
            275             280             285

gaa gct tca aac tta aaa ctt tca caa cgt cgt gcg gaa aca gta gct    912
Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala
            290             295             300

aac tac atc gtt tct aaa ggt gct ccg gca gct aac gta act gca gta    960
Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val
305             310             315             320

ggt tac ggt gaa gca aac cct gta acc ggc gca aca tgt gac aaa gtt    1008
Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val
            325             330             335

aaa ggt cgt aaa gca tta atc gct tgc tta gca ccg gat cgt cgt gtt    1056
Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val
```

241

gaa gtt caa gtt caa ggt act aaa gaa gta act atg taa   1095
Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met
        355   360

<210> 151
<211> 364
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 151
Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val
 1   5   10   15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala
            20   25   30

Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys
        35   40   45

Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr
    50   55   60

Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly
65   70   75   80

Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser
                85   90   95

Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala
            100   105   110

His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp
            115   120   125

Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr
    130   135   140

Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln
145   150   155   160

Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu
                165   170   175

Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala
            180   185   190

Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp
        195   200   205

Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala
    210   215   220

Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser
225   230   235   240

Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala
            245   250   255

Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu

242

```
                260                    265                    270
    Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys
            275                    280                    285

    Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala
            290                    295                    300

    Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val
    305                    310                    315                    320

    Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val
                325                    330                    335

    Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val
                340                    345                    350

    Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met
                355                    360
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<210> 152
<211> 1110
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> Omp5

<220>
<221> CDS
<222> (1)..(1107)

<400> 152

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atg aaa aaa tca tta gtt gct tta gca gta tta tcg gct gca gca gta    48
Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
 1               5                   10                  15

gct caa gca gct cca caa caa aat act ttc tac gca ggt gcg aaa gtt    96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
            20                  25                  30

ggt caa tca tca ttt cac cac ggt gtt aac caa tta aaa tct ggt cac   144
Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
            35                  40                  45

gat gat cgt tat aat gat aaa aca cgt aag tat ggt atc aac cgt aac   192
Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
        50                  55                  60

tct gta act tac ggt gta ttc ggc ggt tac caa atc tta aac caa aat   240
Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
 65                  70                  75                  80

aac ttc ggt tta gca gct gaa tta ggc tat gac tac tac ggt cgc gta   288
Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val
                85                  90                  95

cgt ggt aac gta gat gaa ttc cgt aca gtt aaa cac tct gct cac ggt   336
Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
            100                 105                 110
```

243

```
tta aac tta gcg tta aaa cca agc tac gaa gta tta cct gac tta gac    384
Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
        115             120             125

gtt tac ggt aaa gta ggt att gcg gtt gtt cgt aat gac tat aaa aaa    432
Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys
        130             135             140

tat ggt gcg gaa aac act aac gaa tca aca aca aaa ttc cac aaa tta    480
Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu
145             150             155             160

aaa gca tca act att tta ggt gca ggt gtt gag tac gca att ctt cct    528
Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
        165             170             175

gaa tta gcg gca cgt gtt gaa tac caa tac tta aac aaa gcg ggt aac    576
Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
        180             185             190

tta aat aaa gca tta gtt cgt tca ggc aca caa gat gtg gac ttc caa    624
Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
        195             200             205

tat gct cct gat atc cac tct gta aca gca ggt tta tca tac cgt ttc    672
Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
        210             215             220

ggt caa ggc gct gta gca cca gtt gtt gag cca gaa gtt gta act aaa    720
Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
225             230             235             240

aac ttc gca ttc agc tca gac gtt tta ttt gat ttc ggt aaa tca agc    768
Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
        245             250             255

tta aaa cca gca gca gca aca gct tta gac gca gct aac act gaa atc    816
Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
        260             265             270

gct aac tta ggt tta gca act cca gct atc caa gtt aac ggt tat aca    864
Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
        275             280             285

gac cgt atc ggt aaa gaa gct tca aac tta aaa ctt tca caa cgc cgt    912
Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
        290             295             300

gca gaa act gta gct aac tac tta gtt tct aaa ggt caa aac cct gca    960
Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
305             310             315             320

aac gta act gca gta ggt tac ggt gaa gca aac cca gta acc ggc gca    1008
Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
        325             330             335

aca tgt gat gca gtt aaa ggt cgt aaa gca tta atc gct tgc tta gca    1056
Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
        340             345             350

ccg gat cgt cgt gtt gaa gtt caa gta caa ggt gct aaa aac gta gct    1104
Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
```

244

atg taa   1110
Met

<210> 153
<211> 369
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 153
Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
1   5   10   15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
            20   25   30

Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
        35   40   45

Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
    50   55   60

Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
65   70   75   80

Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val
                85   90   95

Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
            100   105   110

Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
            115   120   125

Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys
    130   135   140

Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu
145   150   155   160

Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
                165   170   175

Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
            180   185   190

Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
            195   200   205

Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
    210   215   220

Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
225   230   235   240

Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
                245   250   255

Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
            260   265   270

```
Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
        275             280             285

Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
        290             295             300

Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
305             310             315             320

Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
            325             330             335

Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
            340             345             350

Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
        355             360             365

Met
```

```
<400> 154
aat att aaa gaa ttc gta aaa gaa gcg ggt aaa ccg cgt tgg gat tgg    48
Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
 1               5                  10                  15

gtt gcg ccg gaa ccg aat acc gca tta atc aac caa gtt aaa gcg tta    96
Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu
             20                  25                  30

gcg gaa gcg cgt atc ggc gat gcg tat cgt att aca gaa aaa caa gcg   144
Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala
             35                  40                  45

cgt tac gaa caa atc gat gca att aaa gcg gat gtt atc gca caa tta   192
Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu
     50                  55                  60

acc gca caa gac gaa acc gtt tct gaa ggt gcg att att gat att att   240
Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile
 65                  70                  75                  80

acc gca tta gaa agt tct att gtt cgc ggt cgt att att gcc ggc gaa   288
Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu
                 85                  90                  95

ccg cgt att gac ggt cgt acg gta gat acg gtt cgt gca tta gac att   336
Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile
             100                 105                 110
```

```
tgc acc ggc gta tta cct cgt acg cac ggt tct gca atc ttt act cgc      384
Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg
        115                 120                 125

ggt gaa aca caa gca tta gcg gtt gca acc tta ggt act gag cgc gat      432
Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp
        130                 135                 140

gca caa att gtt gac gaa tta acc ggc gag aaa tca gac cgt ttc tta      480
Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu
145                 150                 155                 160

ttc cac tat aac ttc cct ccg tac tct gtc ggt gaa acc ggt cgt atc      528
Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile
                165                 170                 175

ggt tcg ccg aaa cgt cgt gaa atc ggc cac ggt cgt tta gcg aaa cgc      576
Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg
                180                 185                 190

ggt gta tta gcg gta atg ccg act gct gaa gaa ttc ccg tat gta gtg      624
Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val
        195                 200                 205

cgc gta gta tct gaa att acc gaa tca aac ggt tct tct tca atg gct      672
Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala
        210                 215                 220

tcc gta tgc ggc gca tct tta gcg tta atg gac gca ggc gta ccg att      720
Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile
225                 230                 235                 240

aaa gcg gcg gtt gcg ggt atc gca atg ggc tta gtg aaa gaa gaa gaa      768
Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu
                245                 250                 255

aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc      816
Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly
                260                 265                 270

gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt      864
Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu
        275                 280                 285

caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc      912
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile
        290                 295                 300

gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg      960
Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met
305                 310                 315                 320

gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct     1008
Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro
                325                 330                 335

cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc     1056
Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile
                340                 345                 350

ggt aaa ggc ggt gcg gtt at                                          1076
Gly Lys Gly Gly Ala Val
```

247

<210> 155
<211> 358
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 155

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Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
 1               5                  10                  15

Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu
            20                  25                  30

Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala
            35                  40                  45

Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu
        50                  55                  60

Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile
65                  70                  75                  80

Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu
                85                  90                  95

Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile
            100                 105                 110

Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg
        115                 120                 125

Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp
    130                 135                 140

Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu
145                 150                 155                 160

Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile
            165                 170                 175

Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg
            180                 185                 190

Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val
        195                 200                 205

Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala
    210                 215                 220

Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile
225                 230                 235                 240

Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu
                245                 250                 255

Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly
            260                 265                 270

Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu
        275                 280                 285
```

```
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile
    290                 295                 300

Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met
305                 310                 315                 320

Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro
                325                 330                 335

Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile
                340                 345                 350

Gly Lys Gly Gly Ala Val
        355


<210> 156
<211> 1055
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> potD

<220>
<221> CDS
<222> (1)..(1053)

<400> 156
atg aaa aaa tta gcg ggt tta ttt gca gca ggt tta gcg aca gtt gca     48
Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala
  1               5                  10                  15

tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct     96
Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala
                 20                  25                  30

caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat    144
Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr
            35                  40                  45

gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa    192
Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys
        50                  55                  60

gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta    240
Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu
 65                  70                  75                  80

aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac    288
Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn
                 85                  90                  95

tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat    336
Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp
                100                 105                 110

cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac    384
His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn
            115                 120                 125

aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt    432
```

249

```
              Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly
                      130                 135                 140

              gca ccg ggt atc gca ttt aac tca aat gac tat aag ggc gat gcg ttc      480
              Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe
              145                 150                 155                 160

              act tct tgg ggt gat tta tgg aaa cct gag ttt gcg aat aaa gta caa      528
              Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln
                              165                 170                 175

              tta tta gat gac gca cgt gaa gta ttt aac att gcg tta tta aaa tta      576
              Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu
                          180                 185                 190

              ggt aaa aac cct aat aca acc aat ccg gaa gag att aaa gcg gct tac      624
              Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr
                          195                 200                 205

              gaa gag tta aga aaa tta cgt cca aac gta ctt tct ttc act tca gac      672
              Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp
                      210                 215                 220

              aac cca gcg aac tca ttt atc gca ggt gaa gta tct gta ggt caa tta      720
              Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu
              225                 230                 235                 240

              tgg aac ggt tct gta cgt att gcg aaa aaa gaa caa gcg ccg gta aac      768
              Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn
                              245                 250                 255

              atg gtg ttc cca aaa gaa ggt cct gta ctt tgg gtt gat acg tta gcc      816
              Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala
                          260                 265                 270

              att ccg gcg aat gcg aaa aac aaa gaa aat gcg cat aag tta atc aac      864
              Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn
                          275                 280                 285

              tac tta tta agc gca ccg gtt gcg gaa aaa tta acg tta gaa atc ggt      912
              Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly
                      290                 295                 300

              tat ccg act tca aac gta gaa gcg tta aaa aca tta cca aaa gag att      960
              Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile
              305                 310                 315                 320

              acc gaa gat ccg gca atc tat ccg aca gct gat gtg tta aaa gcg gca     1008
              Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala
                              325                 330                 335

              caa tgg caa gac gat gta ggt aat gca atc gaa ctt tac gaa aaa ta      1055
              Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys
                          340                 345                 350


              <210> 157
              <211> 351
              <212> PRT
              <213> Actinobacillus pleuropneumoniae

              <400> 157
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250

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Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala
 1               5                  10                  15

Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala
            20                  25                  30

Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr
        35                  40                  45

Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys
    50                  55                  60

Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu
65                  70                  75                  80

Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn
            85                  90                  95

Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp
            100                 105                 110

His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn
            115                 120                 125

Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly
    130                 135                 140

Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe
145                 150                 155                 160

Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln
            165                 170                 175

Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu
            180                 185                 190

Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr
            195                 200                 205

Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp
    210                 215                 220

Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu
225                 230                 235                 240

Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn
            245                 250                 255

Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala
            260                 265                 270

Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn
            275                 280                 285

Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly
    290                 295                 300

Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile
305                 310                 315                 320

Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala
            325                 330                 335
```

251

```
Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys
        340                     345                 350


<210> 158
<211> 525
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> rpmF

<220>
<221> CDS
<222> (1)..(522)


<400> 158
atg caa aag gta aaa cta ccc ctc acc att gac cca tat aaa gac gct    48
Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala
  1               5                  10                  15

cag cgt cga atg gat tac gaa ggc tac atc tca cgt agt ctg ctt aat    96
Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn
              20                  25                  30

cgt ttg ggt gaa tct gtg agc aat gtg cta agc gat gca caa gtt act   144
Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr
          35                  40                  45

ctc tcg tta tat atc gat ccg caa cgc tta acc gtt att aaa ggt acg   192
Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr
      50                  55                  60

gcg aca gtg gaa gtg gaa ttc gat tgc caa cga tgc ggt aac ccg ttt   240
Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
 65                  70                  75                  80

aca caa acg ctt gac tgt tcg ttt tgt ttc agt ccg gtg tcc aat atg   288
Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
                 85                  90                  95

gat cag gcg gac aat ttg ccc gaa att tat gaa cca atc gaa gta aac   336
Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
             100                 105                 110

gag ttc ggt gaa gta aat tta cta gat atg atc gaa gat gga ttt atc   384
Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
         115                 120                 125

atc gaa ttg cct cta gtc ccg atg cat agt gaa gaa cac tgt gaa gtg   432
Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
      130                 135                 140

tcc gtg agt gaa cag gtg ttt ggc gaa ttg cct gaa gaa ttg gcg aaa   480
Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
145                 150                 155                 160

aaa cct aac ccg ttc gct gta tta gct aat tta aag aaa aac tag       525
Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
                 165                 170
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252

<210> 159
<211> 174
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 159

Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala
1   5   10   15

Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn
                20   25   30

Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr
            35   40   45

Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr
        50   55   60

Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
65   70   75   80

Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
                85   90   95

Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
                100   105   110

Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
            115   120   125

Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
        130   135   140

Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
145   150   155   160

Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
                165   170

<210> 160
<211> 1302
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> tig

<220>
<221> CDS
<222> (1)..(1299)

<400> 160
atg tca att tct att gaa act tta gaa ggc tta caa cgc cgc gta act   48
Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
1   5   10   15

att acc gta gct gct gat aaa atc gaa gcg gct tac aaa gag caa tta   96
Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
                20   25   30

aaa ggc tat gcg aaa aac gct cgt gta gac ggt ttc cgt aaa ggt aaa   144

253

```
             Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
                      35                  40                  45

gta ccg cac gca att atc gaa caa cgt ttc ggt tta gcg gct cgc caa    192
Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
         50                  55                  60

gac gta tta tcc gat gaa atg caa cgt gcg ttc ttt gat gcg gta atc    240
Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
 65                  70                  75                  80

gct gag aaa att aac ctt gcc ggt cgt cct acc ttc aca ccg aac aac    288
Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
                     85                  90                  95

tac caa ccg agt caa gaa ttc agc ttc act gca act ttt gaa gta ttc    336
Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
                100                 105                 110

ccg gaa gtt gaa tta aaa ggc tta gaa aat atc gaa gtt gaa aaa ccg    384
Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
            115                 120                 125

gtt gta gaa atc aca gaa gct gat tta gac aaa atg atc gat gtg tta    432
Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
        130                 135                 140

cgt aaa caa caa gcg act tgg gct gaa tct caa gca gcg gca caa gcg    480
Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
145                 150                 155                 160

gaa gac cgt gtt gta atc gac ttc gta ggt tct gta gac ggt gaa gag    528
Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
                165                 170                 175

ttt gaa ggc ggt aaa gcg aca gac ttc act tta gca atg ggt caa agt    576
Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
                180                 185                 190

cgt atg atc cct ggt ttt gaa gaa ggt atc gtt ggt cac aaa gcc ggc    624
Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly
                195                 200                 205

gaa caa ttc gat atc gat gtt act ttc cct gaa gaa tac cac gct gaa    672
Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu
            210                 215                 220

aac tta aaa ggt aaa gcg gcg aaa ttc gca att aca ctt aag aaa gta    720
Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val
225                 230                 235                 240

gaa aat atc gta tta cct gaa tta acc gaa gaa ttc gtg aaa aaa ttc    768
Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe
                245                 250                 255

ggt tca gca aaa act gta gaa gat tta cgt gcg gaa att aag aaa aat    816
Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn
                260                 265                 270

atg caa cgt gaa ctt aaa aac gca gta acc gca cgc gtt aaa aac caa    864
Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln
            275                 280                 285
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254

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gta atc aac ggt tta atc gca caa aat gaa att gaa gtg ccg gct gca    912
Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
    290                 295                 300

gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt    960
Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
305                 310                 315                 320

ttc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gcg gaa tta ttc   1008
Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
                325                 330                 335

gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc   1056
Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
            340                 345                 350

gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa   1104
Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
            355                 360                 365

acg att gca gaa atc gct tca gct tac gaa caa ccg gcg gaa gtt gtt   1152
Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
    370                 375                 380

gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta   1200
Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
385                 390                 395                 400

gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta   1248
Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
                405                 410                 415

act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa   1296
Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
                420                 425                 430

ggc taa                                                            1302
Gly
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<210> 161
<211> 433
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 161

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Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
 1               5                  10                  15

Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
            20                  25                  30

Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
        35                  40                  45

Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
    50                  55                  60

Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
65                  70                  75                  80

Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
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255

Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
            100   105   110

Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
            115   120   125

Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
            130   135   140

Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
145   150   155   160

Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
                165   170   175

Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
            180   185   190

Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly
            195   200   205

Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu
            210   215   220

Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val
225   230   235   240

Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe
            245   250   255

Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn
            260   265   270

Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln
            275   280   285

Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
            290   295   300

Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
305   310   315   320

Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
            325   330   335

Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
            340   345   350

Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
            355   360   365

Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
            370   375   380

Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
385   390   395   400

Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
            405   410   415

256

Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
              420   425   430

Gly

<210> 162
<211> 316
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> tRNA-glu

<400> 162
aatattgcgc tcaaatggca aagcggagag catctttaaa tgttgtcccc atcgtctaga   60

ggcctaggac atcgcccttt cacggcggta accggggttc gaatccccgt ggggacgcca 120

tttaaagatg acttttgttg tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180

tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240

agctgaacaa aagcagctaa gtgtttagtt gaataaagta tcgcgttgaa tgcgttcaaa 300

taaaatttga aaatat   316

<210> 163
<211> 85
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> tRNA-leu

<400> 163
gctctggtgg tggaattggt agacacgcta tcttgagggg gtagtgtcca taggatgtgc   60

gagttcgagt ctcgcccaga gcacc   85

<210> 164
<211> 623
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> yaeE

<220>
<221> CDS
<222> (1)..(621)

<400> 164
atg caa gaa ctc aca cct caa atg tgg ggc tta gtc ggc act tca acg   48
Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr
  1   5   10   15

ctt gaa acg ctc tat atg ggc ttt gcg gcg act tta ctt gct gtg gta   96
Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val

257

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gtc ggt ttg ccg atc ggt ttt ctg gca ttt tta acc ggt aaa gga gag   144
Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu
        35                  40                  45

att tta gag aat ccg cgt tta cat caa gta tta gat gtg att att aat   192
Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn
        50                  55                  60

atc ggt cgt tcc gta ccg ttt att att ttg tta gtc gtg ttg tta cct   240
Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro
65                  70                  75                  80

ttt acg cgt tta ttg gtc ggg aca acg ctc ggt act acg gcg gcg att   288
Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile
                85                  90                  95

gtg ccg tta agc gtt tcg gca att ccg ttt ttt gcg cgt tta act tca   336
Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser
                100                 105                 110

aat gcg tta tta gaa atc cca gca ggt tta acc gaa gcg gcg aaa tcg   384
Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser
        115                 120                 125

atg ggc gca acg aat tgg caa gtg gtc agt aaa ttt tat tta ccg gaa   432
Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu
        130                 135                 140

tca ctg ccg att tta atc aat ggt atc aca tta act tta gtc gct tta   480
Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu
145                 150                 155                 160

atc ggt tat tcg gca atg gcg ggt gcg gtc ggc ggc ggc ggt ttg ggt   528
Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly
                165                 170                 175

aac ctt gcc atc agt tac ggt gaa cac cga aat atg gtc tat gta aaa   576
Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys
                180                 185                 190

tgg atc tca aca att att atc gta gcg att gtg atg atc agt caa aa    623
Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln
                195                 200                 205
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<210> 165
<211> 207
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 165
Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr
 1               5                   10                  15


Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val
            20                  25                  30


Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu
        35                  40                  45
```

258

```
Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn
    50                  55                  60

Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro
65                  70                  75                  80

Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile
                85                  90                  95

Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser
            100                 105                 110

Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser
            115                 120                 125

Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu
    130                 135                 140

Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu
145                 150                 155                 160

Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly
                165                 170                 175

Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys
                180                 185                 190

Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln
    195                 200                 205
```

259